

e.//3.9e-49:282:93//U14572

R-nnnnnnnnnnnnnnn

R-THYR01000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//1.9e-20:215:77//AL031005

R-THYR01000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//1.2e-06:227:64//AC004069

R-THYR01000684

R-THYR01000699

R-THYR01000712

R-THYR01000734//Human BAC clone RG191D16, complete sequence.//3.7e-14:468:64//AC002460

R-THYR01000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533

R-THYR01000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//I25660

R-THYR01000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:175:66//AL034558

R-THYR01000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey sequence.//1.2e-81:391:99//AQ038226

R-THYR01000787//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//9.4e-07:494:58//AC004617

R-THYR01000793

R-THYR01000796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING DRAFT SEQUENCE.//1.7e-42:379:79//Z93014

R-THYR01000805//Human Chromosome 11 pac pDJ610i20, WORKING DRAFT SEQUENCE, 18 unordered pieces.//4.7e-40:362:76//AC002555

R-THYR01000815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//4.0e-58:295:92//Z82199

R-THYRO1000829//Sequence 7 from patent US 5716622.//0.97:362:61//I87788

R-THYRO1000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence.//3.3e-57:522:76//AC004738

R-THYRO1000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//4.2e-17:291:69//AC005849

R-THYRO1000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs, complete sequence.//1.1e-41:419:75//AL031592

R-THYRO1000865//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549

R-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380F5, WORKING DRAFT SEQUENCE.//3.7e-111:569:96//AL031719

R-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0e-97:554:92//AC006015

R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.6e-109:566:94//AF079529

R-THYRO1000934//Homo sapiens full length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378

R-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//8.9e-61:479:81//AC004229

R-THYRO1000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//M28639

R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//AF047440

R-THYRO1000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//AC006126

R-THYRO1000983//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//0.99:71:78//AC005562

R-THYRO1000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 cont

aining uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6  
.7e-42:320:84//AC006078

R-THYRO1000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome X  
p11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z8  
4466

R-THYRO1001003//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey s  
equence.//2.5e-39:310:83//AQ253727

R-THYRO1001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome X  
p11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z8  
4466

R-THYRO1001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 20  
07J14, genomic survey sequence.//5.1e-26:143:100//B56677

R-THYRO1001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2  
386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882

R-THYRO1001093

R-THYRO1001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complet  
e sequence.//0.47:102:73//AC005070

R-THYRO1001120

R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//  
8.9e-81:429:94//AJ006417

R-THYRO1001133//CIT-HSP-2381I10.TR CIT-HSP Homo sapiens genomic clone 23  
81I10, genomic survey sequence.//4.7e-12:237:67//AQ111077

R-THYRO1001134

R-THYRO1001142//H.sapiens CpG island DNA genomic MseI fragment, clone 81  
d1, reverse read cpg81d1.rtl1a.//0.95:214:60//Z56037

R-THYRO1001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cos  
mid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6  
e-26:262:77//B04145

R-THYRO1001177

R-THYRO1001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973

R-THYRO1001204

R-THYRO1001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581

R-THYRO1001262//Homo sapiens, clone hRPK.16\_A\_1, complete sequence.//8.7e-53:442:79//AC006227

R-THYRO1001271//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630

R-THYRO1001290

R-THYRO1001313//H.sapiens CpG island DNA genomic MseI fragment, clone 19 5h3, forward read cpg195h3.ft1b.//0.046:126:66//Z57783

R-THYRO1001320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207

R-THYRO1001321//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558

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R-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288

R-THYRO1001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92//B05884

R-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10 q25, complete sequence.//1.8e-109:584:94//AC005660

R-THYRO1001374

R-THYRO1001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953

R-THYRO1001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequenc



e.//8.7e-38:307:82//AC002377

R-THYRO1001405

R-THYRO1001406//RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297

R-THYRO1001411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123

R-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553

R-THYRO1001434//Microcentus caryae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877

R-THYRO1001458//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578

R-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-99:517:95//AC006001

R-THYRO1001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085

R-THYRO1001534//HS\_2242\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326

R-THYRO1001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//0.42:323:60//AL023876

R-THYRO1001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-42:370:78//AC005077

R-THYRO1001559//Homo sapiens 12q24.2 PAC RPCI5-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868

R-THYRO1001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic

sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308

R-THYR01001573//M.avium rpsL gene.//0.98:131:66//X80120

R-THYR01001584//A.longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653

R-THYR01001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808

R-THYR01001602//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//4.4e-13:320:67//AC005919

R-THYR01001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249

R-THYR01001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:448:92//AJ002190

R-THYR01001637//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 688G8, WORKING DRAFT SEQUENCE.//5.4e-41:381:78//AL031671

R-THYR01001656//HS\_2201\_B2\_A08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence.//0.096:162:63//AQ293168

R-THYR01001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:62//U22954

R-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//4.8e-110:562:95//AJ225089

R-THYR01001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence.//1.5e-17:224:68//AQ042426

R-THYR01001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072

R-THYR01001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011

R-THYR01001721//, complete sequence.//1.3e-101:571:92//AC005500

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R-THYRO1001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//1.1e-15:193:70//AC004777

R-THYRO1001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3.//0.54:260:61//M88244

R-THYRO1001772//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156

R-THYRO1001793

R-THYRO1001809//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE.//2.5e-43:486:74//AL031728

R-THYRO1001854//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//5.0e-41:245:87//AC005696

R-THYRO1001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence.//4.4e-12:419:61//AC005137

R-THYRO1001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCR Region, complete sequence.//8.1e-35:340:78//AC000075

R-VESEN1000122//Homo sapiens Human mRNA, complete cds.//1.3e-23:138:98//AF009368

R-Y79AA1000013

R-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//9.9e-112:551:97//AC006027

R-Y79AA1000037//CIT-HSP-2334F3.TR CIT-HSP Homo sapiens genomic clone 2334F3, genomic survey sequence.//0.16:308:60//AQ036673

R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.1e-56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5.//0.64:203:63//D21079

R-Y79AA1000131//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0548N01; HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered

pieces.//7.0e-18:169:79//AC004795

R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.1e-106:474:98//AL031864

R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78:97//B68074

R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//6.5e-59:386:90//AC004854

R-Y79AA1000230//Cytauxzoon felis 18S ribosomal RNA.//1.0:167:62//L19080

R-Y79AA1000231//HS\_3009\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=0, genomic survey sequence.//6.4e-52:348:88//AQ090225

R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127:65//D10558

R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7e-40:300:84//Z98047

R-Y79AA1000313//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136:83//Z92540

R-Y79AA1000328

R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189:65//X54107

R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300:81//X84692

R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protei

n pseudogene, EST, GSS, complete sequence.//5.7e-45:403:80//AL022163  
R-Y79AA1000368  
R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI  
-11-16B12, genomic survey sequence.//0.10:171:65//B88000  
R-Y79AA1000410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 92N15, WORKING DRAFT SEQUENCE.//4.1e-50:361:83//Z93097  
R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozo  
ite surface protein 5, merozoite surface protein 2, and adenylosuccinat  
e lyase genes, complete cds.//0.071:474:57//AF033037  
R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence.//1.8e-8  
6:221:90//AC005033  
R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complet  
e sequence.//2.1e-14:179:72//AC004057  
R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//4.5e-43:321:83//AC005282  
R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequen  
ce.//0.0012:275:59//AC006143  
R-Y79AA1000540//Z.diploperennis repetitive DNA (clone ZEAR 260).//0.0017  
:258:62//X53609  
R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X1497  
2  
R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete seque  
nce.//0.96:224:61//AC002325  
R-Y79AA1000627//Homo sapiens full length insert cDNA ZA77G02.//6.3e-100:  
533:94//AF075117  
R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7,  
genomic survey sequence.//4.6e-88:429:98//AQ268433  
R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA  
, complete cds.//2.7e-112:586:95//AF093670

R-Y79AA1000748

R-Y79AA1000752

R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316:86//AQ005014

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-17:107:100//D87433

R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00034:520:55//AC005505

R-Y79AA1000794//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 989H11, WORKING DRAFT SEQUENCE.//0.015:322:60//Z83851

R-Y79AA1000800//M.musculus tex264 mRNA (3' region).//1.1e-06:104:78//X80427

R-nnnnnnnnnnnnn//CIT-HSP-2295G6.TF CIT-HSP Homo sapiens genomic clone 2295G6, genomic survey sequence.//0.67:152:62//AQ007605

R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//3.1e-26:423:68//U73642

R-Y79AA1000824//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING DRAFT SEQUENCE.//1.1e-08:449:61//Z97832

R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds.//1.0:101:69//AF083344

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds.//0.40:386:59//U85647

R-Y79AA1000962//CIT-HSP-2298N11.TR CIT-HSP Homo sapiens genomic clone 2298N11, genomic survey sequence.//0.00019:253:65//AQ013111

R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//1.7e-58:446:80//U38253

R-Y79AA1000969

R-Y79AA1000976//CIT-HSP-2350C4.TF CIT-HSP Homo sapiens genomic clone 235

0C4, genomic survey sequence.//3.3e-60:295:100//AQ061422  
R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:34  
8:76//U05823  
R-Y79AA1001023  
R-Y79AA1001041  
R-Y79AA1001048  
R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10,  
complete sequence.//1.2e-60:537:78//AC004626  
R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from 5q12, complete seque  
nce.//2.3e-41:405:77//AC005031  
R-Y79AA1001077  
R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Canc  
er Institute Human PAC Library) complete sequence.//2.0e-09:534:59//AC00  
4801  
R-Y79AA1001105//Staphylococcus epidermidis trimethoprim resistance plasmid  
pSK639.//0.0072:309:63//U40259  
R-Y79AA1001145//RPCI11-59N12.TK RPCI11 Homo sapiens genomic clone R-59N1  
2, genomic survey sequence.//3.7e-07:256:64//AQ200068  
R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndr  
ome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.55:223:61//AP00001  
2  
R-Y79AA1001177//Human gene for Gi3 alpha protein, intron 7 through exon  
9, variant U6 gene, and snRNP E protein pseudogene LH87.//7.0e-09:203:69  
//X54048  
R-Y79AA1001185  
R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Can  
cer Institute Human BAC Library) complete sequence.//2.1e-32:277:81//AC0  
05912  
R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.9

8:325:59//U47924

R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone  
: MAB16, complete sequence.//0.0034:378:59//AB018112

R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5  
unordered pieces.//0.19:106:72//AC004988

R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequ  
ence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)  
).//3.4e-109:549:95//AJ005892

R-Y79AA1001281

R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y  
17126

R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymeras  
e pseudogene, partial cds.//0.0070:284:58//U45372

R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic sur  
vey sequence.//0.11:125:70//AL025355

R-Y79AA1001384//W.makrii mitochondrial CYTB and tRNA genes.//0.070:209:6  
5//X66594

R-Y79AA1001391//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL1P2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745

R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R29144, comp  
lete sequence.//0.99:241:63//AC004221

R-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer  
Institute Human PAC Library) complete sequence.//0.25:81:80//AC005924

R-Y79AA1001493

R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12  
Contains ESTs and GSSs, complete sequence.//1.3e-35:207:95//AL034430

R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53  
) , complete cds.//2.7e-44:285:81//D14336

R-nnnnnnnnnnnnn//Human DNA sequence from clone 113J7 on chromosome Xp11.2



2-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574

R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151

R-Y79AA1001555

R-Y79AA1001585

R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X; contains STS.//6.6e-19:241:76//Z94722

R-Y79AA1001603//H.sapiens CpG island DNA genomic MseI fragment, clone 72 f8, forward read cpg72f8.ft1a.//3.3e-21:131:96//Z62766

R-Y79AA1001613

R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS119 2 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975

R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008

R-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743

R-nnnnnnnnnnnnn//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792

R-Y79AA1001696//Apis mellifera-ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178

R-Y79AA1001705

R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139

R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402

R-nnnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044

R-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//2.3e-90:  
557:89//U74297

R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome  
6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternati  
vely spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MA  
PK p38beta LIKE protein. Contains ESTs, STSS and two predicted CpG islan  
ds, complete sequence.//2.1e-34:306:78//Z95152

R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I14369

R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clon  
e: K23L20, complete sequence.//0.0089:527:58//AB016874

R-Y79AA1001874

R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X8965  
0

R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-2  
6.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related  
, matrix associated, actin dependent regulator of chromatin, subfamily a  
, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains  
ESTs, STSS and GSSs, complete sequence.//1.0:138:68//AL022577

R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA./  
/0.71:153:67//X04465

R-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
lone 172B20, WORKING DRAFT SEQUENCE.//1.0:178:64//AL022319

R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 u  
nordered pieces.//6.3e-49:377:81//AC005011

R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-3  
2:174:99//L77612

R-Y79AA1002103//CIT-HSP-2328I21.TR CIT-HSP Homo sapiens genomic clone 23  
28I21, genomic survey sequence.//1.9e-44:245:96//AQ044502

R-Y79AA1002115//CITBI-E1-2514F10.TF CITBI-E1 Homo sapiens genomic clone

2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752  
R-Y79AA1002125//RPCI11-15J6.TV RPCI-11 Homo sapiens genomic clone RPCI-1  
1-15J6, genomic survey sequence.//8.5e-21:147:91//B75354  
R-Y79AA1002139  
R-Y79AA1002204  
R-nnnnnnnnnnnnn//Human ankyrin G (ANK-3) mRNA, complete cds.//0.040:319:5  
9//U13616  
R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4)./  
/0.99:106:65//X65415  
R-Y79AA1002210  
R-Y79AA1002211//H.sapiens NGAL gene.//1.0:311:59//X99133  
R-Y79AA1002220//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from MAL4P1, WORKING DRAFT SEQUENCE.//5.9e-07:535:57//AL034557  
R-Y79AA1002229  
R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.  
1e-117:564:98//AB014592  
R-Y79AA1002246  
R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-92:453:9  
7//AB013384  
R-Y79AA1002298//HS\_3071\_B2\_E08\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=3071 Col=16 Row=J, genomic survey  
sequence.//1.9e-56:384:87//AQ171331  
R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.  
5e-108:403:99//AB014534  
R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173I12 map 10  
q25, complete sequence.//1.1e-07:368:61//AC005887  
R-Y79AA1002351  
R-Y79AA1002361//H.sapiens CpG island DNA genomic MseI fragment, clone 65  
b9, reverse read cpg65b9.rtl1a.//0.57:59:79//Z62206

R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete  
sequence.//2.0e-98:385:99//AC005920

R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complet  
e sequence.//5.4e-59:490:76//AC004662

R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC l  
ibrary) complete sequence.//6.3e-08:103:80//AC004087

R-Y79AA1002431

R-nnnnnnnnnnnnn//Mouse transcriptional control element.//0.064:84:71//M17  
284

R-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323),  
complete sequence.//1.6e-103:525:96//AC006116

R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complet  
e sequence.//9.7e-38:302:83//AC006238

R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B  
).//0.23:266:61//X95276

【 0 8 2 7 】

相同性検索結果データ 4.

5' 末端クローン配列に対するHuman Unigene相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのTitle、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069

F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete  
cds//0.82:170:64//Hs.2864:L40157

F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U836

68

F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078  
 F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247  
 F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HE  
 LICASE PRP22 [*Saccharomyces cerevisiae*]//0.00019:192:65//Hs.7900:W22411  
 F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759  
 F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910  
 F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734  
 F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p1  
 10delta mRNA, complete cds//0.27:342:61//Hs.14207:U86453  
 F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8  
 e-169:791:98//Hs.27197:AB018340  
 F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4  
 e-37:243:88//Hs.2397:Z70200  
 F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is nov  
 el. [*H.sapiens*]//5.3e-80:383:98//Hs.135552:AI215187  
 F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//  
 2.1e-07:265:63//Hs.85313:AF071309  
 F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079  
 F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYP  
 ROTEIN [*H.sapiens*]//1.3e-18:111:96//Hs.163863:W28729  
 F-HEMBA1000185//*H.sapiens* ERF-2 mRNA//1.0:125:68//Hs.78909:U07802  
 F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:AI240133  
 F-HEMBA1000201//Human In11 mRNA, complete cds//6.5e-75:440:92//Hs.155626  
 :U04847  
 F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529  
 F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//  
 Hs.8136:U81984  
 F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, co  
 mplete cds//1.3e-05:311:64//Hs.81248:U63289

F-HEMBA1000231  
F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377  
F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703  
F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460  
F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562  
F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568  
F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186  
F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406  
F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664  
F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:A1206095  
F-HEMBA1000303  
F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946  
F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:A1124898  
F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965  
F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//Hs.79299:D86961  
F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317:80//Hs.99189:X84712  
F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frames//0.020:334:59//Hs.23094:M19503  
F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61//Hs.78344:AF001548  
F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802  
F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:78//Hs.154326:D42087  
F-HEMBA1000366//ESTs//0.025:56:87//Hs.141629:H74010  
F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433

:58//Hs.159899:AC004853

F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878

F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320

F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15//2.3e-141:712:95//Hs.22900:AC004520

F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//Hs.139088:AF070533

F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.2e-26:351:70//Hs.138992:C14008

F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915

F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:AI079253

F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:AI032875

F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA 0501//7.6e-31:616:66//Hs.159897:AB007970

F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034

F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398

F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.37953:X66893

F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:AI032875

F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590

F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853

F-HEMBA1000469

F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//0.15:253:58//Hs.104640:AF000561

F-HEMBA1000490//Homo sapiens kinectin mRNA, complete cds//0.71:539:56//Hs.82709:Z22551

F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970

F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312:77//Hs.5247:AF029750

F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)//1.3e-08:57:100//Hs.155095:D13666

F-HEMBA1000505//Homo sapiens KE04p mRNA, complete cds//1.0:197:62//Hs.131962:AF064093

F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646

F-HEMBA1000518

F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:AI281881

F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans cDNA CEE SB82F [C.elegans]//2.9e-16:132:84//Hs.155871:AA533783

F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//2.1e-25:192:87//Hs.22383:R51067

F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H.sapiens]//2.4e-57:288:97//Hs.116022:AA455706

F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:153:88//Hs.113283:AF018080

F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809

F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.088:581:57//Hs.65436:U24389

F-HEMBA1000545//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//7.8e-106:731:83//Hs.139107:K00629

F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//Hs.77495:D87684

F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729

F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8e-64:665:72//Hs.137168:AB018303

F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:AI338977

F-HEMBA1000568//EST//0.12:270:61//Hs.134833:AI091046

F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchored protein p137//3.8e-19:409:62//Hs.119283:Z48042



F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681

F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy c  
hain [C.elegans]//7.7e-41:217:96//Hs.55084:AA479162

F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e  
-44:228:97//Hs.155218:AJ007509

F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H.sapiens]//1.7  
e-27:463:65//Hs.13794:AA203241

F-HEMBA1000594//Human clone 230971 defective mariner transposon Hsmar2 m  
RNA sequence//4.0e-68:574:79//Hs.159176:U92019

F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:AI092535

F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7  
e-120:561:99//Hs.5003:AB007925

F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68/  
/Hs.153563:AF011333

F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.col  
i]//7.4e-22:166:84//Hs.26252:AA643235

F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1  
e-138:639:99//Hs.60103:AB014590

F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174

F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582

F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:AI123912

F-HEMBA1000673//H.sapiens mRNA for translin associated protein X//1.7e-4  
7:366:79//Hs.96247:X95073

F-HEMBA1000682//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878

F-HEMBA1000686

F-HEMBA1000702

F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309

F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:AI039850

F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630

F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:AI281881  
 F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491  
 F-HEMBA1000747  
 F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:AI091568  
 F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:H52716  
 F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239  
 F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803  
 F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535216  
 F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300  
 F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536  
 F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542  
 F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367  
 F-HEMBA1000843  
 F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X  
 69962  
 F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572  
 F-HEMBA1000867  
 F-HEMBA1000869//ESTs//5.1e-33:166:77//Hs.141186:R99609  
 F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237  
 F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047  
 F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660  
 F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154  
 F-HEMBA1000910//Human DNA sequence from clone 1409 on chromosome Xp11.1-  
 11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a  
 alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6  
 -Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. C  
 ontains ESTs, STSs and genomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z  
 98046  
 F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537

F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142

F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:AB011119

F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens]//9.4e-10:77:93//Hs.111445:H00596

F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens]//0.0039:54:92//Hs.58338:AA609476

F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase//0.93:132:66//Hs.82285:X54199

F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNIN G ENTRY !!!! [H.sapiens]//0.080:128:71//Hs.118972:AA761369

F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161

F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI127903

F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775

F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314

F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.3e-05:424:59//Hs.159564:AF061936

F-HEMBA1000985//Homo sapiens mRNA, chromosome 1-specific transcript KIAA0492//0.0036:389:60//Hs.127338:AB007961

F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132

F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895

F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835

F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.46468:U45984

F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529

F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:AB007937

F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572

F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238

F-HEMBA1001022

F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.159897:AB007970

F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142

F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515

F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881

F-HEMBA1001052//EST//0.94:149:67//Hs.131216:AI017971

F-HEMBA1001059//N-ACETYLGALACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159479:U06088

F-HEMBA1001060//ESTs//6.8e-14:150:78//Hs.24821:AA044813

F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420

F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//Hs.147802:R71297

F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172

F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248

F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284

F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017

F-HEMBA1001099

F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4e-6

1:341:85//Hs.5247:AF029750  
 F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497  
 F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.  
 066:649:56//Hs.5347:AB007940  
 F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.  
 5e-10:231:68//Hs.27349:AB007917  
 F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747  
 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.  
 2e-73:527:77//Hs.159277:AB018341  
 F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.  
 020:141:65//Hs.7482:AB014582  
 F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457  
 F-HEMBA1001174//ESTs//1.4e-63:363:92//Hs.132798:AA922226  
 F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.mu  
 sculus] //5.0e-54:555:71//Hs.55165:AA573499  
 F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463  
 F-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57  
 //Hs.48824:D87717  
 F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:AI369694  
 F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748  
 F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058  
 F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7  
 647:M94046  
 F-HEMBA1001265  
 F-HEMBA1001281  
 F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL0  
 21155  
 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5  
 .1e-30:530:64//Hs.154050:AC004131

F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741

F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs.155464:AF088219

F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:AI129590

F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201

F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873

F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301

F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:L20861

F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108734:AI073427

F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013

F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569

F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358

F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794

F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074

F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156

F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353

F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-132:643:97//Hs.124217:AA020848

F-HEMBA1001388

F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660

F-HEMBA1001398

F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117  
 F-HEMBA1001407//ESTs//0.53:390:57//Hs.150447:AI017798  
 F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108  
 F-HEMBA1001413  
 F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605  
 F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040  
 F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726  
 F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducibl  
 e), polypeptide 2//1.2e-74:469:80//Hs.1361:M55053  
 F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031  
 F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.mu  
 sculus]//6.8e-47:550:71//Hs.55165:AA573499  
 F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIP1) mRNA, com  
 plete cds//0.82:312:58//Hs.7019:AB005666  
 F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107  
 F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412  
 F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:8  
 8//Hs.40100:AB002390  
 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2  
 e-104:489:99//Hs.14409:AB011144  
 F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451  
 F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs  
 .155464:AF088219  
 F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853  
 :X98054  
 F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5  
 e-105:773:82//Hs.23094:M19503  
 F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902  
 F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869

F-HEMBA1001526  
 F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476  
 F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580  
 F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652  
 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205  
 F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814  
 F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:AJ012449  
 F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184  
 F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228  
 F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988  
 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918  
 F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210  
 F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400  
 F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870  
 F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNIN  
 G ENTRY !!!! [H.sapiens]//0.038:198:64//Hs.34579:AI338536  
 F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899  
 F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204  
 F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560  
 F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283  
 F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121  
 F-HEMBA1001661  
 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:669:99//Hs.107254:AC005943



F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0484//2.0e-57:447:79//Hs.158095:AB007953

F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788

F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060

F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760

F-HEMBA1001709//EST//0.85:131:65//Hs.131451:AI023995

F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:AI302836

F-HEMBA1001712//EST//0.26:214:59//Hs.159088:AI383114

F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL  
PRECURSOR [Rattus norvegicus]//3.0e-30:195:92//Hs.132948:AA194452

F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554

F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101  
524:U58197

F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363

F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415

F-HEMBA1001744//EST//8.7e-77:420:92//Hs.133226:AI052250

F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37  
:300:62//Hs.10887:AB013924

F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328

F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapien  
s]//0.76:218:60//Hs.135553:N41598

F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//  
Hs.98776:AC005622

F-HEMBA1001784//Homo sapiens mRNA for KIAA0474 protein, complete cds//6.  
4e-09:265:67//Hs.158232:AB007943

F-HEMBA1001791

F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570

F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817

F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.

8e-07:439:59//Hs.266:U06233

F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0500//2.5e-175:809:98//Hs.118164:AB007969

F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305

F-HEMBA1001815

F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA,  
partial cds//4.9e-80:842:70//Hs.158174:U66561

F-HEMBA1001820//EST//0.057:214:62//Hs.148715:AI223845

F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//  
6.7e-42:510:65//Hs.66392:AF064244

F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//  
5.2e-13:253:68//Hs.85313:AF071309

F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//  
Hs.6151:D87078

F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.155243:N70293

F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:6  
8//Hs.6833:AB002324

F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.  
8e-185:865:98//Hs.78946:AB014517

F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121

F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSY  
LTRANSFERASE PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:AI141  
922

F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:3  
67:95//Hs.15423:T84036

F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0484//5.4e-86:835:76//Hs.158095:AB007953

F-HEMBA1001896

F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds/

/0.43:114:71//Hs.6133:U94346

F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633

F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:200:62//Hs.9573:AF027302

F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511

F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141

F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:855:99//Hs.154934:AF000145

F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295

F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221

F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882

F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943

F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360

F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.30:85:69//Hs.25674:AF072242

F-HEMBA1001962//ESTs//0.0012:289:59//Hs.125492:AA938930

F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708

F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.

2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive iso-  
log of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178

F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732

F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100

F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581

F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palm-  
aris et plantaris)//9.8e-09:294:63//Hs.99936:X14487

F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803:W63582

F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64  
//Hs.78867:M93426

F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545  
:U32907

F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827

F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057

F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens]//4.5e-26:223:81//Hs.105292:AA504776

F-HEMBA1002084

F-HEMBA1002092

F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) m  
RNA, complete cds//5.6e-21:124:96//Hs.101842:L32832

F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09  
:434:62//Hs.135102:AI190276

F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973

F-HEMBA1002119

F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802

F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393

F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:6  
0//Hs.79170:D86980

F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6  
e-06:353:62//Hs.23741:AB018263

F-HEMBA1002151

F-HEMBA1002153//EST//0.014:328:60//Hs.149115:AI244695

F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0507//5.6e-49:303:79//Hs.158241:AB007976

F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-  
40:616:67//Hs.929:M57965

F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.4  
4766:AJ007590

F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs  
.155464:AF088219

F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//  
Hs.114808:AF026245

F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141

F-HEMBA1002189//EST//5.1e-24:193:81//Hs.163161:AA778363

F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.2  
7:382:59//Hs.21992:AB014589

F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0501//1.2e-14:199:72//Hs.159897:AB007970

F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696

F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767

F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculu  
s]//1.6e-47:251:96//Hs.59906:AA001281

F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0488//2.4e-57:375:71//Hs.67619:AB007957

F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80/  
/Hs.43681:AL022394

F-HEMBA1002237//EST//0.044:137:66//Hs.144448:AA812455

F-HEMBA1002241

F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887

F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, com  
plete cds//1.1e-152:731:97//Hs.159564:AF061936

F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420

F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA,  
complete cds//1.0:395:60//Hs.150926:AF017445

F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404

F-HEMBA1002321//Homo sapiens oxidized low-density lipoprotein receptor m  
RNA, complete cds//0.17:338:60//Hs.77729:AB010710

F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982

F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//  
Hs.154326:D42087

F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8  
e-187:872:98//Hs.6162:AB018314

F-HEMBA1002348//EST//1.0e-19:285:70//Hs.121860:AA776692

F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996

F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mR  
NA, complete cds//2.4e-189:872:99//Hs.119023:AF092563

F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216

F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144

F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:  
97//Hs.25527:AC005954

F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLI  
C PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W271  
41

F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.9079  
8:U79289

F-HEMBA1002439//EST, Weakly similar to-LINE-1 REVERSE TRANSCRIPTASE HOMO  
LOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561

F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.  
sapiens]//1.3e-71:346:98//Hs.136121:W26490

F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160

F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit pr  
ecursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783

F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:  
92//Hs.154583:D50912

F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89  
631:U48508

F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8  
e-45:331:83//Hs.6189:AB011133

F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235

F-HEMBA1002495

F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161

F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74/  
/Hs.19949:X98173

F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:46  
0:83//Hs.113283:AF018080

F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein ( JM21)//9.0e-159:738:98//Hs.6764:AJ011972

F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795

F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951

F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete  
cds//6.1e-46:238:87//Hs.10458:AF088219

F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138  
:655:98//Hs.68900:AF016903

F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//  
Hs.102137:U31875

F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.000  
20:603:57//Hs.20912:AB012162

F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205

F-HEMBA1002561//Human clone 23574 mRNA sequence//4.7e-17:268:72//Hs.7938  
5:U90905

F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete  
cds//4.3e-142:457:99//Hs.151411:AF075587

F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like facto

r, complete cds//2.8e-30:156:100//Hs.32170:AB015132  
 F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159  
 F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363  
 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4  
 e-176:820:99//Hs.20141:AB011169  
 F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013  
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.  
 2e-189:632:97//Hs.91338:AB018351  
 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65  
 //Hs.125129:AB002334  
 F-HEMBA1002629//Human density enhanced phosphatase-1 mRNA, complete cds/  
 /1.3e-07:473:61//Hs.1177:U10886  
 F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390  
 F-HEMBA1002651  
 F-HEMBA1002659//Human vascular endothelial growth factor related protein  
 VRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142  
 F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4  
 e-122:781:85//Hs.23094:M19503  
 F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497  
 F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368  
 F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP ga  
 ted 1 (alpha)//0.00096:418:61//Hs.1323:S42457  
 F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1)  
 mRNA, partial cds//1.8e-11:541:60//Hs.124161:AF065164  
 F-HEMBA1002696//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e  
 -06:345:61//Hs.155647:AC004221  
 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.  
 0e-12:327:62//Hs.13245:AB007924  
 F-HEMBA1002712



F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800

F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521

F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGS T3) mRNA, complete cds//0.21:157:66//Hs.111811:AB007867

F-HEMBA1002742//EST//0.97:138:60//Hs.160545:AI271596

F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372

F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786

F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817

F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126

F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947

F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809

F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392

F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326

F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756

F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938

F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185

F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744

F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119

F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:AI279904

F-HEMBA1002833

F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550

F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823  
 F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEE  
 D8.8 IN CHROMOSOME II [C.elegans] //4.9e-18:110:94//Hs.13322:AA151730  
 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AI279429  
 F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679  
 F-HEMBA1002921  
 F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001  
 F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915  
 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6  
 e-174:803:99//Hs.14687:AB011148  
 F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:G  
 enBank Accession Number M95564 [H.sapiens] //8.1e-36:256:85//Hs.36899:AA1  
 30053  
 F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1  
 .1e-05:479:59//Hs.74019:X83703  
 F-HEMBA1002944//Human putative endothelin receptor type B-like protein m  
 RNA, complete cds//0.83:326:58//Hs.27747:U87460  
 F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.126762:AA913925  
 F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099  
 F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092  
 F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828  
 F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219  
 F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-  
 homolog phosphodiesterase E4)//1.5e-37:247:89//Hs.188:L20971  
 F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mR  
 NA, partial cds//1.7e-05:797:58//Hs.50758:AF092564  
 F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525  
 F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs  
 .155464:AF088219

F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486  
 F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:33  
 0:78//Hs.113283:AF018080  
 F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.15942  
 5:AJ001454  
 F-HEMBA1003037//EST//0.53:59:74//Hs.148011:AI268003  
 F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:33  
 7:95//Hs.105907:AA186514  
 F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-sub  
 unit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182  
 F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438  
 F-HEMBA1003067  
 F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1)  
 mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164  
 F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62  
 //Hs.48998:AB007865  
 F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454  
 F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461  
 F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881  
 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721  
 F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.  
 musculus]//0.98:216:61//Hs.97865:AA405872  
 F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721  
 F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802  
 F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//  
 Hs.12432:AF070575  
 F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.0  
 38:288:63//Hs.6162:AB018314  
 F-HEMBA1003136

F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279  
 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99  
 //Hs.63931:AJ005670  
 F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.  
 1e-24:171:83//Hs.141874:AB014588  
 F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740  
 F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' r  
 egion [E.coli]//4.7e-20:118:97//Hs.118831:AA211895  
 F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523  
 F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135  
 F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412  
 F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:15  
 4:85//Hs.113283:AF018080  
 F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765  
 F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784  
 F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310  
 F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012  
 F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0005  
 4:432:58//Hs.132206:AF039694  
 F-HEMBA1003250  
 F-HEMBA1003257//Homo sapiens fibroblast growth factor-18 (FGF18) mRNA, c  
 omplete cds//4.3e-08:426:64//Hs.49585:AF075292  
 F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991  
 F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020  
 F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864  
 F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867  
 F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransfer  
 ase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662  
 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.

6e-167:799:98//Hs.12836:AB011109  
 F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912  
 F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160  
 F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.105486:AA521012  
 F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189:865:99//Hs.124224:AB001872  
 F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:X99459  
 F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254  
 F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328  
 F-HEMBA1003330  
 F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:78//Hs.146395:AB002329  
 F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTG, and RAD23A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092  
 F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159  
 F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819  
 F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637  
 F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017  
 F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552  
 F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488  
 F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813  
 F-HEMBA1003403//Adducin 2 (beta) {alternative products} //5.0e-05:445:61//Hs.90951:U43959  
 F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309  
 F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546

F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962

F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:686:99//Hs.25812:AF058696

F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60//Hs.47822:AB002378

F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08:775:58//Hs.3847:U59632

F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578

F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16:321:60//Hs.13999:AB014600

F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443

F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:78//Hs.22271:D26067

F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811

F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5.0e-75:736:73//Hs.505:U07559

F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311

F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6e-33:562:64//Hs.81469:U01833

F-HEMBA1003556

F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122

F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327

F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0e-58:455:66//Hs.101448:U35113

F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972

F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546

F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:108:99//Hs.18420:AA599232

F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:9

2//Hs.57937:W68285

F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405

F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827

F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916

F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory prote in HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782

F-HEMBA1003617//Homa sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344

F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:AF077954

F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750

F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159

F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudd ge ne product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591

F-HEMBA1003640//ESTs//1.1e-11:267:66//Hs.34359:AI122791

F-HEMBA1003645

F-HEMBA1003646

F-HEMBA1003656

F-HEMBA1003662

F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381

F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906

F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204

F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H. sapiens]//1.6e-100:478:98//Hs.118866:AI017072

F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691

F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187

F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.8  
1:254:62//Hs.32316:AB011116

F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995

F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760

F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//  
Hs.91916:AF035317

F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921

F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839

F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6  
e-102:753:81//Hs.23094:M19503

F-HEMBA1003742//Homo sapiens chromosome 19, cosmid R31180//0.16:242:62//  
Hs.153325:AC005390

F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946

F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//  
Hs.8136:U81984

F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920

F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//1.7e-24:224  
:81//Hs.18171:AA524327

F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172

F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064

F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3)  
mRNA, complete cds//0.13:222:61//Hs.89230:AF031815

F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239

F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:  
M88108

F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721

F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3  
e-85:586:87//Hs.6051:AB014516

F-HEMBA1003836//EST//6.8e-06:98:74//Hs.145447:AI204220



F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN  
G ENTRY !!!! [H.sapiens]//3.8e-40:151:88//Hs.139007:H74314

F-HEMBA1003856//ESTs//8.6e-53:286:95//Hs.116645:AI005167

F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66/  
/Hs.21355:AB002367

F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.  
3e-30:580:63//Hs.27621:U52840

F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.895  
63:D32002

F-HEMBA1003880

F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2  
e-18:302:67//Hs.23711:AB018295

F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN  
VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.2e-49:295:92//Hs.114673:  
W72675

F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236

F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.0  
81:345:58//Hs.78494:AB011097

F-HEMBA1003926//EST//2.5e-32:253:83//Hs.132635:AI032875

F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:  
69//Hs.154668:AB002389

F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562

F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]//0  
.0029:222:61//Hs.144236:W52380

F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055

F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:  
66//Hs.2076:M29580

F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
ENTRY !!!! [H.sapiens]//2.1e-44:243:76//Hs.91146:N73230

F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567  
 F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI138965  
 F-HEMBA1003978  
 F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009  
 F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456  
 F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//0.022:349:58//Hs.104640:AF000561  
 F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468  
 F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493  
 F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573  
 F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:AI379721  
 F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.2e-51:359:84//Hs.15519:AB018315  
 F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:AI239930  
 F-HEMBA1004042//EST//0.00088:272:61//Hs.155763:AI312281  
 F-HEMBA1004045//EST//2.7e-20:408:66//Hs.162529:AA584160  
 F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M60315  
 F-HEMBA1004049//ESTs//8.1e-68:430:86//Hs.146307:AA584638  
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457:58//Hs.82837:L13435  
 F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.5e-46:199:80//Hs.46328:D87942  
 F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426  
 F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107  
 F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M28713  
 F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.3e-39:335:79//Hs.46468:U45984

F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610:61//Hs.80712:D86957

F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064

F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:AI419759

F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.00055:343:62//Hs.5923:X82260

F-HEMBA1004143

F-HEMBA1004146

F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI186056

F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.8e-15:591:60//Hs.159277:AB018341

F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649:97//Hs.59988:AF067855

F-HEMBA1004199

F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:AI375427

F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays] //1.2e-35:205:94//Hs.10092:AI189282

F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040

F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748

F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514

F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans] //0.012:156:67//Hs.163588:AI073878

F-HEMBA1004238

F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571

F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522

F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds//1.1e-28:295:72//Hs.56205:U96876

F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553:60//Hs.83634:U52112

F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.  
9e-73:490:77//Hs.141874:AB014588

F-HEMBA1004272

F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444

F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118:65//  
Hs.155313:AB002331

F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.  
0:364:56//Hs.118738:AB018343

F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA  
, complete cds//6.9e-187:868:99//Hs.101766:AF022795

F-HEMBA1004289

F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484

F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:AI270047

F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:AI336314

F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452:65//  
Hs.69740:U09367

F-HEMBA1004323//EST//0.44:134:64//Hs.145464:AI204532

F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.  
.017:209:64//Hs.43627:U35612

F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062

F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888

F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.  
49:80:73//Hs.139648:AB014606

F-HEMBA1004341

F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cd  
s//2.7e-39:270:86//Hs.80686:D89667

F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3  
e-46:190:92//Hs.27424:U75968

F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.

3022:D85376

F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens] //7.8e-10:396:61//Hs.33688:AA020928

F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800

F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019

F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250

F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818

F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199

F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin. [H.sapiens] //1.4e-20:144:88//Hs.121076:AI246426

F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531

F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219

F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080

F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606

F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984

F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450

F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600

F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431

F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-89:758:76//Hs.23094:M19503

F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans] //1.4e-61:296:99//Hs.114622:AA693492

F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800

F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//H  
s.76279:X53416

F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381

F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.  
74:74:75//Hs.87497:U90552

F-HEMBA1004554

F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331

F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802

F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2  
e-17:334:67//Hs.24536:AA479825

F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1e-35:337:78//Hs.78160:AF0  
10238

F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661

F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft)  
mRNA, complete cds//0.42:186:66//Hs.84136:U70370

F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606

F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198

F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178

F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416

F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891

F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780

F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522

F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083

F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796

F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582

F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141

F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252

F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.6

4:313:61//Hs.118578:X80821

F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73  
//Hs.155174:AB007892

F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515

F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:  
244:57//Hs.99975:X55019

F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328  
:60//Hs.68900:AF016903

F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5  
.9e-32:476:70//Hs.116874:AA524909

F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515

F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugatin  
g enzyme E2 similar to Drosophila bendless gene product, complete cds//0  
.16:329:58//Hs.75355:D83004

F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0  
e-61:663:71//Hs.23094:M19503

F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813

F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504

F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.000  
20:521:59//Hs.91400:AB006626

F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84/  
/Hs.153563:AF011333

F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e  
-24:416:65//Hs.76460:U49082

F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds  
//1.2e-136:769:91//Hs.153088:L39060

F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.155657:M61120

F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5  
e-115:909:78//Hs.23094:M19503

F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139

F-HEMBA1004771

F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235

F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106

F-HEMBA1004795

F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952

F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971

F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042

F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646

F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481

F-HEMBA1004847//ESTs//2.1e-09:66:98//Hs.158161:AA312511

F-HEMBA1004850//EST//0.033:253:64//Hs.158782:AI376601

F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150

F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987

F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077

F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633

F-HEMBA1004889//Growth arrest-specific 1//0.20:146:68//Hs.65029:L13698

F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304

F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106

F-HEMBA1004918//EST//0.78:122:61//Hs.145491:AI254348

F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172

F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X5



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F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959

F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331

F-HEMBA1004934

F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981

F-HEMBA1004954//ESTs//0.014:404:60//Hs.11177:AA417813

F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478

F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274

F-HEMBA1004972

F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:AB007914

F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946

F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013

F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750

F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589

F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026

F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429

F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356

F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548

F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560

F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237

F-HEMBA1005039//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627

F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, comple

te cds//0.078:442:59//Hs.100602:AF010193

F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802

F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462

F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587

F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381

F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785

F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105

F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561

F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916

F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304

F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106

F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875

F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021

F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216

F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914

F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197

F-HEMBA1005202

F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436

F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547

F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081

F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302

F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp

lete cds//6.0e-54:399:79//Hs.129735:AF010144  
 F-HEMBA1005244//ESTs//2.5e-14:85:100//Hs.128744:AI191922  
 F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896  
 F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7  
 e-151:705:98//Hs.72660:AB011157  
 F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380  
 F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777  
 F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//  
 Hs.12451:U97018  
 F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232  
 F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs  
 .155464:AF088219  
 F-HEMBA1005311  
 F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516  
 F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615  
 F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117  
 F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.0007  
 5:310:63//Hs.111597:U68723  
 F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:  
 97//Hs.129361:AJ007581  
 F-HEMBA1005353//EST//5.4e-09:222:68//Hs.119508:AA485732  
 F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88/  
 /Hs.151689:U09414  
 F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.  
 5e-70:572:73//Hs.43265:AF071787  
 F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905  
 F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mR  
 NA//6.1e-43:341:81//Hs.154069:U06452  
 F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI193053

F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448  
 F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans] //1.0e-130:620:98//Hs.108990:N25951  
 F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans] //7.7e-151:727:97//Hs.17118:AI033807  
 F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513  
 F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347  
 F-HEMBA1005411  
 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248  
 F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323  
 F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259:72//Hs.89897:U28687  
 F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783  
 F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107  
 F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:L37368  
 F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481:92//Hs.23094:M19503  
 F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219  
 F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:AF039694  
 F-HEMBA1005497//Glucocorticoid receptor alpha {alternative products} //8.7e-41:588:69//Hs.102761:U25029  
 F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318:73//Hs.159530:AC004957  
 F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635

F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911  
F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:  
79//Hs.153014:AB002353  
F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.mel  
anogaster]//5.3e-76:378:97//Hs.22767:N99220  
F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7  
) gene, complete cds//0.54:623:56//Hs.143551:AF048693  
F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575  
F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.  
1e-55:288:85//Hs.144563:AF057280  
F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs  
.155464:AF088219  
F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cer  
evisiae]//1.2e-30:166:96//Hs.17035:AI080471  
F-HEMBA1005530  
F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-ma  
f) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376  
F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461  
F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903  
F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257  
F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507  
F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9  
e-128:610:98//Hs.77738:AB007932  
F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873  
F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64  
//Hs.57929:AB011538  
F-HEMBA1005582  
F-HEMBA1005583  
F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381

F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS//0.

54:439:59//Hs.2137:D49357

F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:5

7//Hs.7720:AB002323

F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609

F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982

F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.

2e-22:721:61//Hs.144563:AF057280

F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae] //1.8e-89:454:96//Hs.19400:AA662845

F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535

F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734

F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199

F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956

F-HEMBA1005666

F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.

7e-45:255:79//Hs.114293:AB011142

F-HEMBA1005679//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//

1.2e-37:356:77//Hs.139107:K00629

F-HEMBA1005680

F-HEMBA1005685

F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406

F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678

F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143

F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//2.6e-

20:151:88//Hs.77393:D14697

F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754

F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024  
 F-HEMBA1005755//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//  
 1.8e-48:425:78//Hs.103948:K00627  
 F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs  
 .155464:AF088219  
 F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141  
 F-HEMBA1005813//ESTs//0.012:209:63//Hs.113365:R77747  
 F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds/  
 /2.0e-07:439:62//Hs.6133:U94346  
 F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577  
 F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788  
 F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9  
 e-42:690:66//Hs.23094:M19503  
 F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//H  
 s.79706:U53204  
 F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150  
 F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
 0484//1.4e-53:332:83//Hs.158095:AB007953  
 F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097  
 F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete  
 cds//7.2e-45:411:77//Hs.46468:U45984  
 F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.000  
 54:477:59//Hs.37125:U42766  
 F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081  
 F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HP  
 X42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006  
 F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger prot  
 ein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880  
 F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588

F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883  
F-HEMBA1005963  
F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516  
F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530  
F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526  
F-HEMBA1006002  
F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151  
F-HEMBA1006031  
F-HEMBA1006035  
F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080  
F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.141186:R99609  
F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.143321:AI139422  
F-HEMBA1006081  
F-HEMBA1006090//EST//1.2e-12:340:62//Hs.161195:AI418788  
F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313  
F-HEMBA1006100//ESTs//7.1e-22:273:73//Hs.144407:AA737799  
F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741  
F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968  
F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222  
F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372  
F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734  
F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881  
F-HEMBA1006155  
F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575



F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627  
 F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117  
 F-HEMBA1006198//ESTs//0.017:133:67//Hs.142168:AA292540  
 F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98/  
 /Hs.109268:AF070557  
 F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.  
 7647:M94046  
 F-HEMBA1006252  
 F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706  
 F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.  
 00037:158:69//Hs.159277:AB018341  
 F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631  
 F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140  
 F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770  
 F-HEMBA1006283  
 F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964  
 F-HEMBA1006291  
 F-HEMBA1006293  
 F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA,  
 complete cds//0.76:416:58//Hs.46465:U45285  
 F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3  
 e-49:637:68//Hs.37656:AB011174  
 F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350  
 F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789  
 F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142  
 F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.mel  
 anogaster] //5.3e-76:378:97//Hs.22767:N99220  
 F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287  
 F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107

:X59244

F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026

F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422:59//Hs.80667:AF010233

F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922

F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531

F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503

F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477

F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881

F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830

F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835

F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264

F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194

F-HEMBA1006445

F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889

F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124:AF019369

F-HEMBA1006467

F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:AI091453

F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257:AA875998

F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081

F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532

F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897

F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.128621:AA910431

F-HEMBA1006492

F-HEMBA1006494//ESTs//8.5e-24:299:72//Hs.153413:AI248625  
F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389  
F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072  
F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:AB014566  
F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli] //3.9e-98:483:97//Hs.94811:AA011185  
F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002  
F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI160081  
F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654:98//Hs.21301:AF093419  
F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638  
F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898  
F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425  
F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136  
F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.144372:AI346522  
F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479  
F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778  
F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219  
F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB018295  
F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862  
F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875  
F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION [S.cerevisiae] //2.5e-75:379:97//Hs.40911:AI391502

F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI343331  
 F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589  
 F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185  
 F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:AA505003  
 F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196:U40282  
 F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615  
 F-HEMBA1006653  
 F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189  
 F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317  
 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065  
 F-HEMBA1006676  
 F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575  
 F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145  
 F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198  
 F-HEMBA1006708  
 F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545  
 F-HEMBA1006717//ESTs//2.6e-31:286:78//Hs.55573:W37226  
 F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105  
 F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087  
 F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129727:AF035587

F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576:56//Hs.149323:AB002325

F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs.141073:W72720

F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657

F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250

F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798

F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503

F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298

F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III [C.elegans]//4.8e-110:523:98//Hs.125790:AA287723

F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:AI051551

F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624

F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970

F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327

F-HEMBA1006865

F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN I N ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938

F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214

F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592

F-HEMBA1006914//EST//0.065:366:62//Hs.162914:AA666199

F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989

F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154764:U16258

F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539  
F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712  
F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382  
F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein/  
/4.4e-92:437:98//Hs.42644:AJ010841  
F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6  
940:Z48633  
F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete c  
ds//1.8e-144:740:94//Hs.14934:AF004828  
F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sia  
lyltransferase//1.9e-79:447:89//Hs.75268:X74570  
F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968  
F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723  
F-HEMBA1007002  
F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282  
F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mR  
NA, complete cds//2.5e-78:827:70//Hs.43003:AF035812  
F-HEMBA1007045  
F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659  
F-HEMBA1007052  
F-HEMBA1007062  
F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212  
F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845  
F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//  
6.7e-75:417:91//Hs.80510:M74002  
F-HEMBA1007080  
F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-0  
6:568:61//Hs.1974:M92432  
F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA,

complete cds//0.95:541:57//Hs.3828:U49260  
 F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595  
 F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354  
 F-HEMBA1007121//ESTs//3.5e-69:335:98//Hs.140519:AA643182  
 F-HEMBA1007129  
 F-HEMBA1007147//ESTs//3.2e-07:235:64//Hs.124813:W46172  
 F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136  
 F-HEMBA1007151  
 F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318:97  
 //Hs.22396:AF062085  
 F-HEMBA1007178//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
 ENTRY !!!! [H.sapiens]//4.2e-39:248:90//Hs.157148:AA311921  
 F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965  
 F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.  
 6e-158:478:98//Hs.3363:D86987  
 F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252  
 F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6  
 e-177:839:98//Hs.27197:AB018340  
 F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan sy  
 ndrome)//2.7e-56:647:69//Hs.82314:M31642  
 F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//H  
 s.79706:U53204  
 F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:64//Hs.1  
 2432:AF070575  
 F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//  
 0.99:239:60//Hs.111749:U13695  
 F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836  
 F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:H06475  
 F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529

F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637  
 F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062  
 F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74  
 615  
 F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506  
 F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634  
 F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241  
 F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens] /  
 /3.5e-09:144:76//Hs.20597:W58370  
 F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130  
 F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006  
 F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561  
 F-HEMBA1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568  
 F-HEMBA1000008//H.sapiens mRNA for translin associated protein X//1.1e-4  
 3:370:78//Hs.96247:X95073  
 F-HEMBA1000018//Nuclear factor of kappa light polypeptide gene enhancer  
 in B-cells 1 (p105)//1.0:108:70//Hs.83428:M58603  
 F-HEMBA1000024//EST//5.4e-07:137:70//Hs.125389:AA878307  
 F-HEMBA1000025//EST//0.99:362:58//Hs.121221:AA757392  
 F-HEMBA1000030//H.sapiens mRNA for cylicin II//1.3e-10:525:62//Hs.3232:Z  
 46788  
 F-HEMBA1000036  
 F-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, c  
 omplete cds//6.2e-102:450:98//Hs.20815:AF084928  
 F-HEMBA1000039//EST//0.0034:97:73//Hs.141684:W35358  
 F-HEMBA1000044//ESTs//0.0048:218:63//Hs.123161:AA807319  
 F-HEMBA1000048//EST//0.00025:222:62//Hs.122474:AA765131  
 F-HEMBA1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717  
 F-HEMBA1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3



e-54:259:88//Hs.23094:M19503  
F-HEMBB1000055//ESTs//0.0017:289:62//Hs.125755:AA286923  
F-HEMBB1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9  
e-59:286:84//Hs.93121:AB018304  
F-HEMBB1000083  
F-HEMBB1000089//EST//0.0016:192:66//Hs.137093:AA917621  
F-HEMBB1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645  
F-HEMBB1000103//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//  
4.9e-43:418:74//Hs.103948:K00627  
F-HEMBB1000113//EST//4.6e-23:221:76//Hs.142065:AA173763  
F-HEMBB1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521  
F-HEMBB1000136//ESTs//2.3e-101:507:96//Hs.12659:AA195207  
F-HEMBB1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044  
F-HEMBB1000144//EST//4.5e-52:298:91//Hs.149580:AI281881  
F-HEMBB1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:  
X92715  
F-HEMBB1000175//EST//1.0:101:65//Hs.162898:AA659646  
F-HEMBB1000198//EST//0.99:179:56//Hs.116880:AA662457  
F-HEMBB1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4  
e-15:139:82//Hs.101414:AB011129  
F-HEMBB1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277  
F-HEMBB1000218//EST//0.11:136:63//Hs.134683:AI092013  
F-HEMBB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X6  
9962  
F-HEMBB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y  
08612  
F-HEMBB1000244//ESTs//3.2e-15:139:81//Hs.134549:AI078483  
F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete  
cds//2.1e-156:735:98//Hs.151411:AF075587

F-HEMBB1000258//EST//0.0091:325:60//Hs.97533:AA435884  
 F-HEMBB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4  
 e-33:100:100//Hs.27424:U75968  
 F-HEMBB1000266//Homo sapiens mRNA for myosin phosphatase target subunit  
 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930  
 F-HEMBB1000272//ESTs//1.3e-93:440:99//Hs.109224:N46684  
 F-HEMBB1000274//ESTs//0.41:221:65//Hs.71990:AA151796  
 F-HEMBB1000284//EST//0.00024:108:73//Hs.100725:F13689  
 F-HEMBB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574  
 F-HEMBB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.  
 00092:252:65//Hs.41153:AB018326  
 F-HEMBB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787  
 F-HEMBB1000318//EST//0.014:184:61//Hs.155758:AI311870  
 F-HEMBB1000335//EST//0.99:187:63//Hs.137424:AA243729  
 F-HEMBB1000336//EST//1.0:209:63//Hs.150410:AI003611  
 F-HEMBB1000337//EST//0.086:133:66//Hs.128207:AA972330  
 F-HEMBB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127  
 F-HEMBB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:76//Hs  
 .155464:AF088219  
 F-HEMBB1000341  
 F-HEMBB1000343//EST//0.66:163:63//Hs.150822:AI302729  
 F-HEMBB1000354//ESTs//7.1e-61:292:100//Hs.152266:AA926874  
 F-HEMBB1000369//ESTs, Highly similar to t-BOP [M.musculus]//0.013:157:64  
 //Hs.129982:AI420970  
 F-HEMBB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934  
 F-HEMBB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348  
 F-HEMBB1000391//ESTs//0.033:237:64//Hs.135289:AI092963  
 F-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4  
 e-165:762:98//Hs.16184:AJ001642

F-HEMBB1000402//EST//0.013:291:59//Hs.149191:AI246155  
 F-HEMBB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194  
 F-HEMBB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925  
 F-HEMBB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.129735:AF010144  
 F-HEMBB1000438//ESTs//0.073:446:58//Hs.134632:AI223429  
 F-HEMBB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627  
 F-HEMBB1000449//EST//5.5e-21:356:67//Hs.157848:AI362501  
 F-HEMBB1000455//ESTs//0.092:147:65//Hs.106446:N93227  
 F-HEMBB1000472  
 F-HEMBB1000480//EST//0.98:83:71//Hs.146462:AI124898  
 F-HEMBB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206  
 F-HEMBB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560  
 F-HEMBB1000491  
 F-HEMBB1000493//ESTs//0.019:103:69//Hs.138358:T66178  
 F-HEMBB1000510//Glucocorticoid receptor alpha {alternative products} //1.6e-46:409:77//Hs.102761:U25029  
 F-HEMBB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413  
 F-HEMBB1000523//ESTs//0.69:332:59//Hs.106845:W19543  
 F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710  
 F-HEMBB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens] //7.7e-31:554:67//Hs.157142:U85996  
 F-HEMBB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.158095:AB007953  
 F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.0e-33:537:65//Hs.5444:AB018293  
 F-HEMBB1000564  
 F-HEMBB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001

F-HEMBB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238

F-HEMBB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker type s), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533

F-HEMBB1000589//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091

F-HEMBB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990

F-HEMBB1000592//EST//0.0038:51:88//Hs.148022:AI269323

F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//Hs.3386:AF053356

F-HEMBB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589

F-HEMBB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809

F-HEMBB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864

F-HEMBB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI346481

F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349

F-HEMBB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075

F-HEMBB1000638//EST//0.0076:92:75//Hs.125496:AA883735

F-HEMBB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830

F-HEMBB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778

F-HEMBB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531

F-HEMBB1000665//EST//0.44:152:63//Hs.149534:AI280924

F-HEMBB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2

e-79:280:85//Hs.23094:M19503  
 F-HEMBB1000673//ESTs//0.99:177:59//Hs.149864:N80474  
 F-HEMBB1000684//Protein kinase, interferon-inducible double stranded RNA  
 dependent//2.6e-31:220:87//Hs.73821:M35663  
 F-HEMBB1000693//Homo sapiens neuroanl mRNA, complete cds//5.3e-120:575:9  
 7//Hs.158300:AF040723  
 F-HEMBB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125  
 F-HEMBB1000706//EST//8.6e-14:373:61//Hs.138281:R55703  
 F-HEMBB1000709//EST//0.99:110:65//Hs.162437:AA577510  
 F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56  
 741  
 F-HEMBB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216  
 F-HEMBB1000738//EST//5.9e-13:259:64//Hs.159699:AI417328  
 F-HEMBB1000749//EST//3.1e-42:271:87//Hs.162197:AA535216  
 F-HEMBB1000763  
 F-HEMBB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.  
 melanogaster]//0.021:111:72//Hs.38178:AA921830  
 F-HEMBB1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5e-116:580:  
 97//Hs.5009:AA081390  
 F-HEMBB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//H  
 s.86201:U78876  
 F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//3.  
 0e-65:672:71//Hs.155983:AB014577  
 F-HEMBB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI133727  
 F-HEMBB1000794//ESTs//0.00098:289:59//Hs.138782:N73572  
 F-HEMBB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI298375  
 F-HEMBB1000810//ESTs//0.038:92:71//Hs.148763:AA668871  
 F-HEMBB1000821//EST//0.94:129:62//Hs.162299:AA555154  
 F-HEMBB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421

F-HEMBB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI283069  
F-HEMBB1000827  
F-HEMBB1000831  
F-HEMBB1000835//EST//4.3e-27:201:85//Hs.141451:N29915  
F-HEMBB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948  
F-HEMBB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4  
e-135:875:85//Hs.23094:M19503  
F-HEMBB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:  
61//Hs.311:U00238  
F-HEMBB1000870//EST//0.00091:246:62//Hs.126502:AA913831  
F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//  
Hs.128434:AF085351  
F-HEMBB1000883//ESTs//0.42:107:67//Hs.154173:AI379823  
F-HEMBB1000887  
F-HEMBB1000888//ESTs//1.0:137:67//Hs.8121:AA521290  
F-HEMBB1000890//ESTs//1.0:116:65//Hs.7105:T23433  
F-HEMBB1000893//EST//0.0079:408:58//Hs.146504:AI129834  
F-HEMBB1000908//EST//9.2e-21:205:79//Hs.132635:AI032875  
F-HEMBB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//  
Hs.7938:D86984  
F-HEMBB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049  
F-HEMBB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI095468  
F-HEMBB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089  
F-HEMBB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593  
F-HEMBB1000947  
F-HEMBB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9  
.3e-48:572:72//Hs.2379:U23942  
F-HEMBB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938  
F-HEMBB1000975//ESTs//0.78:180:66//Hs.104789:AA417124

F-HEMBB1000981

F-HEMBB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete  
cds//6.7e-07:308:62//Hs.122967:AF059569

F-HEMBB1000991//EST//0.12:125:66//Hs.22945:R43713

F-HEMBB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055

F-HEMBB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.  
62:193:62//Hs.119004:AB014565

F-HEMBB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025

F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17  
:384:67//Hs.108604:AC002310

F-HEMBB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:2  
84:60//Hs.161547:W04991

F-HEMBB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247

F-HEMBB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61/  
/Hs.129982:AI420970

F-HEMBB1001037//EST//0.0057:192:66//Hs.149987:AI291177

F-HEMBB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721

F-HEMBB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687  
:X96586

F-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.  
0e-42:149:96//Hs.15832:AB014518

F-HEMBB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs  
.155464:AF088219

F-HEMBB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942

F-HEMBB1001063

F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:73  
6:95//Hs.12953:AF034803

F-HEMBB1001096//EST//0.017:154:66//Hs.130403:AA909272

F-HEMBB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293

F-HEMBB1001105//Human BRCA2 region, mRNA sequence CG016//0.30:84:75//Hs.  
112434:U50529

F-HEMBB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61  
ALPHA SUBUNIT [*Canis familiaris*]//9.3e-38:341:77//Hs.14038:R06800

F-HEMBB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062

F-HEMBB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139

F-HEMBB1001119

F-HEMBB1001126

F-HEMBB1001133//H.sapiens mRNA for translin associated protein X//1.2e-2  
8:739:61//Hs.96247:X95073

F-HEMBB1001137

F-HEMBB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:  
69//Hs.146395:AB002329

F-HEMBB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854

F-HEMBB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716

F-HEMBB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863

F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:  
66//Hs.73073:D78334

F-HEMBB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CON  
TAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [*S.cerevisiae*]//1.5e-65:  
312:100//Hs.86878:AA599183

F-HEMBB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:1  
99:64//Hs.74047:X71129

F-HEMBB1001199

F-HEMBB1001208//ESTs//0.12:120:69//Hs.130093:AA928802

F-HEMBB1001209//EST//0.00028:215:65//Hs.118276:W15258

F-HEMBB1001210//EST//2.9e-05:297:60//Hs.88840:AA281452

F-HEMBB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5  
e-37:260:76//Hs.72660:AB011157



F-HEMBB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0507//0.00046:650:58//Hs.158241:AB007976

F-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [M  
us musculus]//6.7e-103:477:100//Hs.127835:AI378790

F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:6  
7//Hs.129918:AB005754

F-HEMBB1001249//EST//0.26:203:63//Hs.140791:AA935909

F-HEMBB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219

F-HEMBB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977

F-HEMBB1001267//Ataxia telangiectasia mutated (includes complementation  
groups A, C and D)//6.1e-24:146:78//Hs.51187:U82828

F-HEMBB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI359248

F-HEMBB1001282//GA-binding protein transcription factor, beta subunit 2  
(47kd)//0.39:531:57//Hs.78915:U13045

F-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK  
353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.1660  
6:W81021

F-HEMBB1001289//ESTs//6.4e-100:467:99//Hs.151720:AI287890

F-HEMBB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sap  
iens]//1.3e-135:654:98//Hs.124217:AA020848

F-HEMBB1001302

F-HEMBB1001304//ESTs//0.98:109:68//Hs.138972:AA047725

F-HEMBB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339

F-HEMBB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs  
.155464:AF088219

F-HEMBB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7  
e-98:625:85//Hs.23094:M19503

F-HEMBB1001326//ESTs//0.00030:257:63//Hs.62208:H12380

F-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:8

7//Hs.43071:AA206222  
 F-HEMBB1001335  
 F-HEMBB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.  
 5e-56:282:87//Hs.15731:AB011135  
 F-HEMBB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:  
 161:65//Hs.132206:AF039694  
 F-HEMBB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878  
 F-HEMBB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.  
 2e-45:176:77//Hs.114293:AB011142  
 F-HEMBB1001356//EST//0.32:292:59//Hs.135771:AI005648  
 F-HEMBB1001364  
 F-HEMBB1001366//EST//7.8e-24:367:69//Hs.138765:N70347  
 F-HEMBB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.  
 .155464:AF088219  
 F-HEMBB1001369//EST//0.17:211:63//Hs.120066:AA707973  
 F-HEMBB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2  
 e-36:225:79//Hs.129748:AB011099  
 F-HEMBB1001384  
 F-HEMBB1001387//ESTs//0.61:215:60//Hs.145915:AI342230  
 F-HEMBB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8  
 e-94:568:83//Hs.23094:M19503  
 F-HEMBB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete  
 cds//0.021:373:58//Hs.125750:AF065988  
 F-HEMBB1001424//EST//0.20:307:58//Hs.135336:AI049827  
 F-HEMBB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//  
 Hs.83466:AF038174  
 F-HEMBB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos tau  
 rus]//5.5e-153:729:96//Hs.21679:AF034175  
 F-HEMBB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:

85//Hs.101996:AB002345

F-HEMBB1001443

F-HEMBB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216

F-HEMBB1001454//ESTs//1.4e-46:279:93//Hs.104866:AA426038

F-HEMBB1001458//EST//1.7e-09:106:83//Hs.141422:N20920

F-HEMBB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220

F-HEMBB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740

F-HEMBB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:AB018303

F-HEMBB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088

F-HEMBB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942

F-HEMBB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815

F-HEMBB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735

F-HEMBB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093

F-HEMBB1001536//ESTs//0.0047:120:68//Hs.144858:R67748

F-HEMBB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306

F-HEMBB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315

F-HEMBB1001562//ESTs//0.95:161:61//Hs.145075:AI208240

F-HEMBB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953

F-HEMBB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080

F-HEMBB1001585  
 F-HEMBB1001586//EST//0.84:132:64//Hs.145264:AI218708  
 F-HEMBB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.9079  
 8:U79289  
 F-HEMBB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414  
 F-HEMBB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680  
 F-HEMBB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314  
 F-HEMBB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713  
 F-HEMBB1001635//ESTs//0.92:282:60//Hs.126980:AA934077  
 F-HEMBB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.  
 116549:AL009172  
 F-HEMBB1001641//EST//0.11:53:81//Hs.112445:AA594279  
 F-HEMBB1001653//EST//0.91:124:64//Hs.144213:T40480  
 F-HEMBB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds  
 //7.0e-13:473:63//Hs.54481:D86407  
 F-HEMBB1001668//ESTs//0.94:83:69//Hs.146202:AI252519  
 F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.  
 3e-172:803:98//Hs.24439:AB014546  
 F-HEMBB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:1  
 00//Hs.106104:AA599496  
 F-HEMBB1001685//EST//2.2e-05:112:73//Hs.130984:AI015430  
 F-HEMBB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6  
 e-08:425:62//Hs.37035:U07664  
 F-HEMBB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398  
 F-HEMBB1001706  
 F-HEMBB1001707//EST//0.091:241:60//Hs.136830:AA769219  
 F-HEMBB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064  
 F-HEMBB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs  
 .155464:AF088219

F-HEMBB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485  
:97//Hs.120581:W25578

F-HEMBB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244

F-HEMBB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144

F-HEMBB1001753//ESTs//0.00013:35:100//Hs.139643:H06263

F-HEMBB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077

F-HEMBB1001760//ESTs//6.5e-06:503:58//Hs.21766:AI357639

F-HEMBB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0507//2.9e-13:498:60//Hs.158241:AB007976

F-HEMBB1001785//EST//0.16:262:60//Hs.162526:AA584102

F-HEMBB1001797//ESTs//0.37:201:63//Hs.91559:AA806370

F-HEMBB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951

F-HEMBB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0487//1.3e-54:311:81//Hs.92381:AB007956

F-HEMBB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017

F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCI  
P1) mRNA, complete cds//7.6e-164:763:98//Hs.159396:AF056209

F-HEMBB1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190

F-HEMBB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:8  
6//Hs.22271:D26067

F-HEMBB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370

F-HEMBB1001850//EST//0.0035:204:61//Hs.7311:T23858

F-HEMBB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:82//Hs  
.155464:AF088219

F-HEMBB1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752

F-HEMBB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371

F-HEMBB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503

F-HEMBB1001872

F-HEMBB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923  
:Y12478

F-HEMBB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box  
protein)//0.32:346:60//Hs.100555:X98743

F-HEMBB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868

F-HEMBB1001899//ESTs//0.17:242:62//Hs.136969:AA830918

F-HEMBB1001905

F-HEMBB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155

F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA  
, complete cds//1.2e-83:672:81//Hs.82210:U47742

F-HEMBB1001910//EST, Weakly similar to albumin [H.sapiens] //0.047:206:62  
//Hs.159777:Z19955

F-HEMBB1001911

F-HEMBB1001915//ESTs//0.92:136:71//Hs.144465:R68882

F-HEMBB1001921//EST//2.0e-19:398:67//Hs.44789:N36113

F-HEMBB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245

F-HEMBB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398

F-HEMBB1001930//EST//0.043:157:63//Hs.161927:AA483904

F-HEMBB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:8  
0//Hs.154326:D42087

F-HEMBB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875

F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:6  
6//Hs.40100:AB002390

F-HEMBB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:3  
84:60//Hs.8546:U97669

F-HEMBB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101

F-HEMBB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//H  
s.96:D90070

F-HEMBB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418

F-HEMBB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053

F-HEMBB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969

F-HEMBB1001973//Myelin oligodendrocyte glycoprotein {alternative products} //2.1e-48:426:78//Hs.53217:Z48051

F-HEMBB1001983

F-HEMBB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051

F-HEMBB1001990//ESTs//0.25:171:64//Hs.7961:AA401205

F-HEMBB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103

F-HEMBB1001997//EST//5.3e-33:294:76//Hs.161041:H82636

F-HEMBB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964

F-HEMBB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093

F-HEMBB1002009//ESTs//0.066:441:58//Hs.125313:AI201685

F-HEMBB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951

F-HEMBB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699

F-HEMBB1002043//ESTs, Weakly similar to T06E6.d [C.elegans] //1.0:217:60//Hs.3487:AA425553

F-HEMBB1002044

F-HEMBB1002045

F-HEMBB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256

F-HEMBB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661

F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:AB014512

F-HEMBB1002069

F-HEMBB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239

F-HEMBB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625

F-HEMBB1002115//EST//0.0083:244:64//Hs.125353:AA877080  
 F-HEMBB1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027  
 F-HEMBB1002139//ESTs//0.64:145:71//Hs.157821:AI362013  
 F-HEMBB1002142//ESTs//0.013:311:59//Hs.150037:AI292214  
 F-HEMBB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254  
 F-HEMBB1002189//EST//0.26:81:70//Hs.147726:AI220208  
 F-HEMBB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.1  
 6:608:58//Hs.4:X03350  
 F-HEMBB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//H  
 s.301:U18934  
 F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:40  
 5:67//Hs.104115:X52332  
 F-HEMBB1002218//EST//0.015:241:61//Hs.105298:AA489813  
 F-HEMBB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs  
 .155464:AF088219  
 F-HEMBB1002247  
 F-HEMBB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HP  
 X42B) mRNA, complete cds//6.8e-47:418:77//Hs.125231:AF068006  
 F-HEMBB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0  
 e-47:437:77//Hs.154872:AB011166  
 F-HEMBB1002255//ESTs//0.017:255:61//Hs.126786:U74314  
 F-HEMBB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA,  
 complete cds//0.17:511:57//Hs.58169:AF017790  
 F-HEMBB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998  
 F-HEMBB1002300  
 F-HEMBB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete  
 cds//6.3e-14:228:72//Hs.46468:U45984  
 F-HEMBB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083  
 F-HEMBB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:39



9:96//Hs.105837:AA536054

F-HEMBB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188

F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein/  
/1.4e-155:724:98//Hs.42644:AJ010841

F-HEMBB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991

F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//  
1.7e-06:66:96//Hs.154762:U00943

F-HEMBB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838

F-HEMBB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796

F-HEMBB1002381

F-HEMBB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//H  
s.2126:L36566

F-HEMBB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784

F-HEMBB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456

F-HEMBB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0501//2.0e-32:371:73//Hs.159897:AB007970

F-HEMBB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.544  
86:X54150

F-HEMBB1002442

F-HEMBB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:7  
7//Hs.154326:D42087

F-HEMBB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101

F-HEMBB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274

F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-  
89:493:92//Hs.159605:U43885

F-HEMBB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA,  
complete cds//0.019:228:63//Hs.74304:AF001691

F-HEMBB1002492//EST//0.24:149:62//Hs.146790:AI149051

F-HEMBB1002495//Fc fragment of IgE, high affinity I, receptor for; beta

polypeptide//1.3e-22:331:71//Hs.30:M89796  
F-HEMBB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494  
F-HEMBB1002509//ESTs//0.017:220:63//Hs.155263:AI273725  
F-HEMBB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354  
F-HEMBB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4  
e-50:580:72//Hs.23094:M19503  
F-HEMBB1002522//EST//0.010:172:62//Hs.147224:AI205719  
F-HEMBB1002531  
F-HEMBB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs  
.155464:AF088219  
F-HEMBB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102  
F-HEMBB1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648  
F-HEMBB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191  
F-HEMBB1002579//EST//1.0:77:68//Hs.147935:AI250286  
F-HEMBB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095  
F-HEMBB1002590//ESTs//0.64:132:63//Hs.155688:AI003657  
F-HEMBB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336  
F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-15  
2:710:98//Hs.129826:AF089749  
F-HEMBB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817  
F-HEMBB1002603//EST//0.10:144:63//Hs.158180:AI367945  
F-HEMBB1002607//ESTs//0.024:345:62//Hs.143304:AI084058  
F-HEMBB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323  
F-HEMBB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711  
F-HEMBB1002614//ESTs//0.0048:136:71//Hs.106280:R13901  
F-HEMBB1002617//EST//0.034:320:59//Hs.41223:H89127  
F-HEMBB1002623//ESTs//0.88:222:60//Hs.129920:AA167217  
F-HEMBB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs  
.151051:U07620

F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811  
 F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680  
 F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679  
 F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124  
 F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674  
 F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504  
 F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992  
 F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor  
 (TACI) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614  
 F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588  
 F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN  
 SUI2-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs  
 .20814:AI242922  
 F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729  
 F-MAMMA1000009//Human c-yes-1 mRNA//1.0e-48:447:77//Hs.75680:M15990  
 F-MAMMA1000019  
 F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750  
 F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945  
 F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739  
 F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461  
 F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculu  
 s]//2.7e-18:330:63//Hs.59906:AA001281  
 F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF  
 F40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019  
 F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840  
 F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:7  
 0//Hs.22271:D26067  
 F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0  
 0013:199:69//Hs.37656:AB011174

F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA  
 , complete cds//1.2e-52:346:77//Hs.90357:U40705

F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792

F-MAMMA1000117

F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508

F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402

F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319

F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843

F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585

F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924

F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050

F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695

F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530

F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657

F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739

F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035

F-MAMMA1000227//ESTs//0.010:268:60//Hs.116412:AA506926

F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913

F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873

F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587

F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543

F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015

F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874

F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087

F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726

F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361

F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505

F-MAMMA1000284

F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087

F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641

F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243

F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529

F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519

F-MAMMA1000313

F-MAMMA1000331

F-MAMMA1000339

F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963

F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892

F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.158095:AB007953

F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503

F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:8

5//Hs.154326:D42087

F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569

F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344

F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:98//Hs.32170:AB015132

F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590

F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503

F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:117:84//Hs.83916:U53468

F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725

F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092

F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111

F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532

F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:AF061573

F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459

F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641

F-MAMMA1000429//Homo sapiens sorting nexin-3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:AF034546

F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830

F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:AB011166

F-MAMMA1000446

F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:93//Hs.9043:W21827

F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase, complete cds//0.58:311:63//Hs.66721:D49818

F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830

F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830

F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948

F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482

F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219

F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878

F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352

F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497

F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352

F-MAMMA1000565

F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//5.8e-51:404:80//Hs.125231:AF068006

F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045

F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780

F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//8.8e-45:390:78//Hs.159523:AF001622

F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744

F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886

F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519

F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091

:300:60//Hs.29207:AF071494

F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478

F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605

F-MAMMA1000623

F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.  
98614:AF006751

F-MAMMA1000643//Homo sapiens nephrocytin (NPHP1) mRNA, partial cds//0.0  
92:365:59//Hs.75474:AF023674

F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353

F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//  
9.0e-30:531:64//Hs.139107:K00629

F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490

F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4  
316:U80743

F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds  
//3.3e-07:249:62//Hs.44481:U13220

F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627

F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081

F-MAMMA1000713//Acetylcholinesterase [I4-E5 doman] [human, tumor cell li  
nes, Genomic, 847 nt]//0.16:84:72//Hs.157124:S71129

F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:61//Hs.274  
14:U79275

F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-  
07:210:66//Hs.71148:AA854648

F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247

F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8  
.1e-22:288:72//Hs.114685:AA700024

F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs  
.22670:AF006513



F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0484//4.8e-40:288:78//Hs.158095:AB007953

F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//  
Hs.1742:L33075

F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:  
802:98//Hs.31575:AF100141

F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580

F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.  
3e-51:323:88//Hs.153468:AB011147

F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494

F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-1  
4:285:68//Hs.162011:AA513663

F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative product  
s} //6.2e-47:341:82//Hs.53217:Z48051

F-MAMMA1000761//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNIN  
G ENTRY !!!! [H.sapiens]//9.8e-19:131:76//Hs.118972:AA761369

F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288

F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114

F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137

F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//  
Hs.12432:AF070575

F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849

F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130

F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089

F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e-48:241:74//Hs  
.155464:AF088219

F-MAMMA1000841

F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA

, complete cds//0.18:483:59//Hs.82210:U47742  
 F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696  
 F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877  
 F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022  
 F-MAMMA1000855  
 F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:3  
 20:59//Hs.71388:AF032906  
 F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135  
 F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342  
 F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.  
 116549:AL009172  
 F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812  
 F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777  
 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59/  
 /Hs.75850:D87459  
 F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147  
 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//1.4e-91:484:94//Hs.138938:AA012894  
 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812  
 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465  
 F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy c  
 hain H3//2.6e-06:211:63//Hs.76716:X67055  
 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683  
 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506  
 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081  
 F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628  
 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239  
 F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,  
 3429 nt]//1.0e-25:312:66//Hs.116007:S79267

F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968

F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785

F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734

F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303

F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714

F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474

F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//Hs.129735:AF010144

F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814

F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096

F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802

F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062

F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007

F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724

F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711

F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:Y15718

F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968

F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds//3.6e-32:753:61//Hs.98384:AF062006

F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857

F-MAMMA1001038

F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178

F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI419882

F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719

F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503

F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585

F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116

F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749

F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503

F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420

F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896

F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254

F-MAMMA1001092//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627

F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045

F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915

F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219

F-MAMMA1001133

F-MAMMA1001139

F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534

F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217

F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741

F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147

F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299  
 F-MAMMA1001181  
 F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA,  
 complete cds//6.5e-47:313:81//Hs.97203:U83171  
 F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083  
 F-MAMMA1001198  
 F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348  
 F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974  
 F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776  
 F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200  
 F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:8  
 4//Hs.154326:D42087  
 F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8  
 e-05:435:59//Hs.30898:AB014534  
 F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587  
 F-MAMMA1001244  
 F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476  
 F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121  
 F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149  
 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.  
 8e-41:659:64//Hs.65238:AB014561  
 F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7  
 e-33:336:74//Hs.23094:M19503  
 F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//H  
 s.21858:U80747  
 F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:7  
 6//Hs.74554:D38522  
 F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832

F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998

F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426

F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305

F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//1.9e-58:295:97//Hs.102336:Z83838

F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087

F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147

F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806

F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197

F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267

F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:75//Hs.109358:AB018258

F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:273:80//Hs.42674:U61981

F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR//4.6e-09:415:58//Hs.839:M86826

F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:67//Hs.61333:D83402

F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763

F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.0:176:64//Hs.82001:U50928

F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80//Hs.43681:AL022394

F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//0.00042:125:75//Hs.46328:D87942

F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:54  
3:71//Hs.37181:D64108

F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321

F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590

F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040

F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053

F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//  
2.0e-24:273:72//Hs.75939:D78335

F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3  
.2e-25:397:68//Hs.116874:AA524909

F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366

F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0  
.99:258:61//Hs.154196:U87269

F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795

F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506

F-MAMMA1001547

F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5  
e-130:614:98//Hs.129937:AB007931

F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.  
sapiens]//0.71:181:62//Hs.118866:AI017072

F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M6  
1764

F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339

F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132

F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375

F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23  
642:U79266

F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152

F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.1

58229:U28727

F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSS and GSSs and genomic markers DXS1003 and DXS1055//1.4e-40:447:73//Hs.154353:AL022165

F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:611:67//Hs.57679:U57796

F-MAMMA1001635

F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524

F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.00069:140:68//Hs.59829:AB014602

F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.015:135:71//Hs.27349:AB007917

F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens] //0.064:472:60//Hs.110819:AI027548

F-MAMMA1001671

F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317

F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889

F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765

F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549

F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, complete cds//8.0e-45:323:83//Hs.46468:U45984

F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548

F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926

F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.5e-111:725:84//Hs.159154:U47634



F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098  
F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768  
F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245  
F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7  
e-67:822:69//Hs.23094:M19503  
F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (HOH  
01) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632  
F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822  
F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109  
F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcr  
ipt, partial//6.6e-41:309:84//Hs.102576:AJ010230  
F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072  
F-MAMMA1001768//Human transcription factor, forkhead related activator 4  
(FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs.96028:AF042832  
F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:68  
6:79//Hs.113283:AF018080  
F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//  
0.00071:392:60//Hs.32981:U38276  
F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940  
F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549  
F-MAMMA1001788//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//  
6.7e-21:212:77//Hs.103948:K00627  
F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72/  
/Hs.5158:AB007869  
F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987  
F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884  
F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:N47096  
F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582  
F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589

F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds//0.082:153:66//Hs.114948:AF059293

F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742

F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691

F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315, complete cds//2.0e-29:641:62//Hs.56808:D88827

F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665

F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028

F-MAMMA1001854

F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218

F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060

F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.084:672:58//Hs.152455:AF044209

F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687

F-MAMMA1001878

F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944

F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576

F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078

F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521

F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874

F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529

F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859

F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:81//Hs.91916:AF035317

F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878

F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sapiens]//7.9e-09:150:72//Hs.118222:N91115

F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633

F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826

F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915  
 F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159  
 F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
 0484//1.2e-54:455:70//Hs.158095:AB007953  
 F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580  
 F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225  
 F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256  
 F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305  
 F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5  
 e-36:382:75//Hs.23094:M19503  
 F-MAMMA1002078  
 F-MAMMA1002082  
 F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012  
 F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partia  
 l//0.54:388:57//Hs.99423:AJ010840  
 F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120  
 F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932  
 F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs  
 .155464:AF088219  
 F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:AI272963  
 F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:H52638  
 F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338  
 F-MAMMA1002145//EST//0.12:204:60//Hs.160983:AI392837  
 F-MAMMA1002153  
 F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335:97/  
 /Hs.88424:AA281385  
 F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD  
 61)//0.99:310:58//Hs.87149:M35999  
 F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196

F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X172  
06

F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:  
U39400

F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:1  
21:98//Hs.146354:Z22548

F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362

F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120

F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk5  
2b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645

F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:AI024063

F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gam  
ma subunit [R.norvegicus]//4.6e-69:344:90//Hs.76822:AI359536

F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, co  
mplete cds//0.99:454:56//Hs.122755:AF032986

F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903

F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:AI308841

F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, compl  
ete cds//1.2e-06:427:61//Hs.69949:M94172

F-MAMMA1002269

F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715

F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440

F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF  
F40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019

F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, comp  
lete cds//4.3e-07:349:64//Hs.92614:M62302

F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460

F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57  
//Hs.77234:AB001914

F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935

F-MAMMA1002308//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] //6.9e-41:293:83//Hs.105292:AA504776

F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA, complete cds//0.0037:173:67//Hs.69423:AF055481

F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-41:473:65//Hs.92381:AB007956

F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291

F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908

F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536

F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515

F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPI P8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026

F-MAMMA1002332//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.2e-26:342:72//Hs.103948:K00627

F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:58//Hs.5333:AB018254

F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6940:Z48633

F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] //3.9e-14:146:81//Hs.163073:R02591

F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907

F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:AI247086

F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539

F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78//Hs.32511:AB007901

F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733

F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818

F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830  
 F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923  
 F-MAMMA1002362//EST//0.25:304:58//Hs.162427:AA576345  
 F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34  
 677  
 F-MAMMA1002384//ESTs//1.1e-05:220:65//Hs.141388:R52022  
 F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-11  
 8:578:97//Hs.25516:AI086362  
 F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624  
 F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632  
 F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737  
 F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745  
 F-MAMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788  
 F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030  
 F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:8  
 3//Hs.154326:D42087  
 F-MAMMA1002446  
 F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809  
 F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6  
 .3e-06:595:59//Hs.99932:L38707  
 F-MAMMA1002470  
 F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, comple  
 te cds//0.018:417:58//Hs.75074:U12779  
 F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059  
 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds/  
 /9.4e-120:560:98//Hs.155223:AF055460  
 F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628  
 F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]  
 //4.0e-07:257:63//Hs.133013:AA604920

F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391  
:L12392

F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214

F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788

F-MAMMA1002554

F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:1  
87:62//Hs.62354:M83822

F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421

F-MAMMA1002571//EST//0.28:115:66//Hs.156768:AI351368

F-MAMMA1002573//ESTs//2.1e-48:265:94//Hs.155128:AI224516

F-MAMMA1002585

F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831

F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:AI334107

F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958

F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220

F-MAMMA1002612//ESTs, Moderately similar to hCDC10 protein [H.sapiens]//  
8.3e-18:353:65//Hs.60895:AA428463

F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357

F-MAMMA1002618

F-MAMMA1002619

F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90  
//Hs.47344:AF041449

F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:N52300

F-MAMMA1002625

F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0507//1.1e-35:355:76//Hs.158241:AB007976

F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-  
05:439:61//Hs.91400:AB006626

F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733  
 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385  
 F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190  
 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:AI393335  
 F-MAMMA1002662//EST//0.99:95:63//Hs.144074:AI005489  
 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64/  
 /Hs.8262:U36336  
 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-0  
 6:272:64//Hs.106070:U22398  
 F-MAMMA1002673  
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.  
 2e-162:752:99//Hs.3363:D86987  
 F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:N69915  
 F-MAMMA1002698//ESTs//2.5e-09:190:68//Hs.138292:AI220397  
 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81  
 //Hs.22396:AF062085  
 F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:AI274697  
 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, comp  
 lete cds//1.1e-51:307:79//Hs.46328:D87942  
 F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:N25041  
 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692  
 F-MAMMA1002727//EST//0.97:137:63//Hs.145153:AI150165  
 F-MAMMA1002728//ESTs, Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC  
 RIBONUCLEASE [Saccharomyces cerevisiae]//2.6e-12:129:81//Hs.154181:AA193  
 502  
 F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853  
 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312  
 F-MAMMA1002748  
 F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848



F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98/  
/Hs.32168:AB007902  
F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293  
F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782  
F-MAMMA1002769  
F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M860  
4 Met protein (M8604 Met) gene//7.6e-84:417:97//Hs.77705:U07563  
F-MAMMA1002780//EST//0.78:210:63//Hs.149413:AI273988  
F-MAMMA1002782  
F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:AI380710  
F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919  
F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:AI378514  
F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2..  
4e-57:286:88//Hs.15731:AB011135  
F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:7  
2//Hs.22271:D26067  
F-MAMMA1002835  
F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE C  
HAIN 1 [Locusta migratoria]//7.7e-38:179:78//Hs.141344:H29951  
F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590  
F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4  
e-137:635:99//Hs.7531:AB018353  
F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:3  
29:58//Hs.107747:AI357868  
F-MAMMA1002858  
F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643  
F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696:78//  
Hs.83987:U09284  
F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423

F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:AI183632  
 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete  
 cds//3.8e-30:680:61//Hs.129732:D45027  
 F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504:6  
 0//Hs.19944:U04270  
 F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657  
 F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666  
 F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265  
 F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.0  
 0053:382:57//Hs.61796:U85658  
 F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952  
 F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125  
 F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730  
 F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapien  
 s] //7.9e-103:485:99//Hs.102928:AI346344  
 F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.  
 6e-194:910:98//Hs.31720:AB014598  
 F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:AI423389  
 F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:AI313418  
 F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:60//Hs  
 .54697:AB007884  
 F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400  
 F-MAMMA1002972  
 F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932  
 F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944  
 F-MAMMA1002987//EST//0.044:254:59//Hs.135014:AI095645  
 F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//  
 3.9e-22:185:83//Hs.62192:J02931  
 F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA

0501//1.0e-16:343:61//Hs.159897:AB007970  
 F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979  
 F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2  
 e-51:620:69//Hs.75258:AF054174  
 F-MAMMA1003013//Human HOX4C mRNA for a homeobox protein//0.73:347:58//Hs  
 .74061:X59372  
 F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062  
 F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:AI374951  
 F-MAMMA1003026//EST//1.0:136:67//Hs.9123:T50137  
 F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549  
 F-MAMMA1003035  
 F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391  
 F-MAMMA1003040//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.5e-9  
 3:339:85//Hs.5247:AF029750  
 F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D13639  
 F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase like protein from C.el  
 egans//1.0:209:60//Hs.99491:Y12336  
 F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742  
 F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518  
 F-MAMMA1003056  
 F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein MD6 [M.  
 musculus]//1.3e-88:334:97//Hs.96500:AI206781  
 F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:AI022618  
 F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5  
 e-51:329:71//Hs.75154:AB014531  
 F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA,  
 complete cds//8.5e-44:288:88//Hs.81008:AF043045  
 F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:21  
 3:60//Hs.42945:Y08136

F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200  
:64//Hs.32950:X82634

F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, complete  
cds//5.4e-27:421:66//Hs.5394:AF105424

F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786

F-MAMMA1003140

F-MAMMA1003146//Homo sapiens mRNA for GALT3 protein//7.2e-82:397:97//Hs.  
151344:Y15062

F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.0  
0019:297:61//Hs.108945:AB011087

F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:48  
7:65//Hs.3847:U59632

F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//H  
s.79706:U53204

F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:9  
2//Hs.82510:D31886

F-NT2RM1000032

F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:  
81//Hs.78442:D83782

F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5  
e-108:542:95//Hs.60103:AB014590

F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//H  
s.79706:U53204

F-NT2RM1000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:3  
53:96//Hs.154980:AA948067

F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA,  
complete cds//0.029:281:59//Hs.46465:U45285

F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210

F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:

97//Hs.3439:AC004472

F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.

8e-116:550:97//Hs.65238:AB014561

F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190  
:63//Hs.431:L13689

F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00  
086:126:70//Hs.92693:AF007155

F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054

F-NT2RM1000127

F-NT2RM1000131

F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subun  
it mRNA, nuclear gene encoding mitochondrial protein, complete cds//3.7e  
-92:448:97//Hs.49767:AF044959

F-NT2RM1000153//Homo sapiens mRNA for MTG8-related protein MTG16a, compl  
ete cds//1.0:546:58//Hs.110099:AB010419

F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00  
081:126:70//Hs.92693:AF007155

F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:AI424382

F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.  
87:454:59//Hs.47061:AF045458

F-NT2RM1000242

F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NA  
P1) mRNA, complete cds//0.97:135:66//Hs.27910:AF049105

F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190

F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248  
:69//Hs.1674:M90516

F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H.sapiens  
]//2.9e-98:530:93//Hs.104650:AI037879

F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:

80//Hs.23106:D50920

F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047

F-NT2RM1000272

F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D  
[Bos taurus]//1.3e-21:308:73//Hs.15071:AA781144

F-NT2RM1000300

F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708  
:92//Hs.5719:D63880

F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e  
-35:182:99//Hs.9837:D79205

F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976

F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798

F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7e-75:3  
87:95//Hs.108619:W28608

F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691

F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.  
sapiens]//7.4e-91:481:95//Hs.163707:AA137181

F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X8050  
7

F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353

F-NT2RM1000399

F-NT2RM1000421

F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, c  
omplete cds//1.2e-85:418:97//Hs.20815:AF084928

F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapiens]//1.  
6e-38:201:97//Hs.106262:AI052382

F-NT2RM1000539//EST//0.070:145:62//Hs.149711:AI284660

F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847

F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:AI359957

F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:58//Hs.79706:U53204

F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//0.98:226:61//Hs.17931:AB006625

F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]//6.2e-51:254:98//Hs.132096:AA314601

F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds//8.5e-55:276:97//Hs.19122:AF038957

F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60//Hs.113936:AB005297

F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:AI188279

F-NT2RM1000672

F-NT2RM1000691//Homa sapiens mRNA for HRIHFB2060, partial cds//7.0e-121:582:98//Hs.146282:AB015348

F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101

F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//1.5e-66:435:85//Hs.5038:AJ004832

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.6e-127:690:92//Hs.147946:AB011139

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2e-68:524:83//Hs.112360:AF027208

F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465

F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:321:63//Hs.150390:AB007885

F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.053:271:60//Hs.139745:U39067

F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frames//6.9e-20:128:94//Hs.23094:M19503

F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845  
 F-NT2RM1000800  
 F-NT2RM1000802  
 F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2e-64:4  
 90:84//Hs.112360:AF027208  
 F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:AI359957  
 F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//0.92:2  
 83:58//Hs.2314:X15422  
 F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:178:67//  
 Hs.1376:U26726  
 F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequence//3.8  
 e-06:384:59//Hs.90314:L05148  
 F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partia  
 l//3.0e-149:726:97//Hs.99423:AJ010840  
 F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643  
 F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//5.3e-5  
 4:277:96//Hs.11125:AI015619  
 F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239  
 F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730)  
 containing the hFEN1 gene//4.0e-155:750:97//Hs.132898:AC004770  
 F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, comple  
 te cds//8.8e-158:762:97//Hs.26285:AF082516  
 F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds//6.  
 3e-19:310:67//Hs.65238:AB014561  
 F-NT2RM1000894  
 F-NT2RM1000898  
 F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:AI268701  
 F-NT2RM1000924//HOMEBOX PROTEIN HOX-A5//0.00051:458:59//Hs.37034:M26679  
 F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cds//0.0



84:386:58//Hs.101474:AB018350  
 F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:299:59//  
 Hs.83419:D87440  
 F-NT2RM1000978  
 F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP) mRNA,  
 complete cds//1.3e-161:760:98//Hs.58488:U97067  
 F-NT2RM1001008//ESTs//1.3e-12:144:75//Hs.133122:AI025200  
 F-NT2RM1001043//EST//0.24:117:64//Hs.161536:N80395  
 F-NT2RM1001044//ESTs, Weakly similar to C43E11.9 [C.elegans]//3.0e-98:49  
 1:96//Hs.102173:AA045270  
 F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:533:57//H  
 s.79706:U53204  
 F-NT2RM1001066//ESTs//1.2e-114:538:99//Hs.129020:AI380703  
 F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//0.69:5  
 86:56//Hs.62354:M83822  
 F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)  
 //0.0019:294:64//Hs.30223:X90846  
 F-NT2RM1001082//Archain//3.9e-37:290:81//Hs.33642:X81198  
 F-NT2RM1001085  
 F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770:68//Hs.74107:  
 X59244  
 F-NT2RM1001102//ESTs//1.2e-35:638:63//Hs.131737:AI343331  
 F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246:63//Hs.75188:U10564  
 F-NT2RM1001112//ESTs//8.9e-82:437:93//Hs.6330:H38495  
 F-NT2RM1001115  
 F-NT2RM1001139//Keratin 9//1.5e-05:518:59//Hs.2783:Z29074  
 F-NT2RM2000006//ESTs//3.9e-16:96:98//Hs.101117:AA576113  
 F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:640:59  
 //Hs.148027:X63563

F-NT2RM2000030  
 F-NT2RM2000032//ESTs//7.1e-18:138:68//Hs.114031:AA700958  
 F-NT2RM2000042//ESTs//0.0091:241:61//Hs.147895:AI286243  
 F-NT2RM2000092  
 F-NT2RM2000093//ESTs//2.6e-40:226:94//Hs.163521:H42085  
 F-NT2RM2000101//ESTs//1.0:235:61//Hs.48860:N27428  
 F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//5.8e-4  
 6:287:88//Hs.77271:X07767  
 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, com  
 plete cds//3.0e-139:566:97//Hs.18953:AF067223  
 F-NT2RM2000192//EST//3.5e-07:168:65//Hs.163122:AA756999  
 F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans]//3.6e-93:489  
 :95//Hs.143499:R72672  
 F-nnnnnnnnnnnnn//ESTs//1.0e-70:269:97//Hs.156175:AI334328  
 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.  
 0e-129:615:98//Hs.111862:AB011162  
 F-NT2RM2000259//ESTs//6.1e-30:172:85//Hs.116406:AA209520  
 F-NT2RM2000260//ESTs//2.5e-25:133:93//Hs.14169:AA203500  
 F-NT2RM2000287//ESTs//6.2e-13:97:83//Hs.118523:H98981  
 F-NT2RM2000322//Interferon regulatory factor 5//0.84:208:61//Hs.54434:U5  
 1127  
 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds//2.  
 8e-176:805:99//Hs.129952:AB011132  
 F-NT2RM2000363//ESTs//1.2e-24:139:96//Hs.48818:N63543  
 F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA  
 , partial cds//3.7e-96:599:86//Hs.75871:U48251  
 F-NT2RM2000371  
 F-NT2RM2000374//ESTs//3.2e-13:98:91//Hs.65853:AI050866  
 F-NT2RM2000395//Growth arrest-specific 1//0.80:129:67//Hs.65029:L13698

F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714:59//Hs.28757:U  
81006

F-NT2RM2000407//ESTs//9.4e-92:458:96//Hs.148873:T33582

F-NT2RM2000420//EST//1.8e-61:296:99//Hs.147186:AI193053

F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transporter, s  
erotonin), member 4//1.5e-06:260:61//Hs.553:L05568

F-NT2RM2000452//ESTs//1.0:132:62//Hs.110004:AI097379

F-NT2RM2000469//ESTs//0.34:249:60//Hs.149575:AI281807

F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.4  
e-16:386:63//Hs.8309:AB018290

F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA, comp  
lete cds//0.99:272:61//Hs.76669:U08021

F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/  
/1.6e-172:824:97//Hs.4812:AF061243

F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.18:313:6  
0//Hs.129725:AF047487

F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]  
//2.7e-41:231:94//Hs.7049:AI141736

F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220

F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs.74369:AF032108

F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.  
89631:U48508

F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128

F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITO  
CHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs.55609:W37993

F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.  
8e-175:820:98//Hs.3363:D86987

F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220

F-NT2RM2000594

F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.0  
17:253:65//Hs.102402:AF040963

F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313

F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548

F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.0  
24:326:59//Hs.6150:AB011093

F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258

F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0  
e-143:664:98//Hs.19542:AB018272

F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4  
e-139:664:98//Hs.7278:AB014558

F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702

F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4  
e-169:518:99//Hs.115763:AB014576

F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:AI337371

F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, com  
plete cds//6.7e-86:746:74//Hs.5321:AF006083

F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:6  
4//Hs.7938:D86984

F-NT2RM2000718//Homa sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:  
594:98//Hs.136058:AB015342

F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107  
:X59244

F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE  
IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464:9  
1//Hs.161551:W24286

F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-8  
2:640:81//Hs.5247:AF029750

F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//

Hs.105919:AB002338

F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:AI346701

F-NT2RM2000951//Homo sapiens XYLb mRNA for xylulokinase, complete cds//2  
.8e-185:847:99//Hs.137580:AB015046

F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanog  
aster] //6.2e-94:441:99//Hs.59075:AI023761

F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//  
Hs.84753:D87433

F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831

F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cer  
evisiae] //2.9e-48:282:93//Hs.17035:AI080471

F-NT2RM2001065

F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding mo  
tif, complete cds//1.7e-08:449:62//Hs.75111:D87258

F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear prot  
ein isoform mRNA, partial cds//0.00079:274:59//Hs.102732:U88153

F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190

F-NT2RM2001141

F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042

F-NT2RM2001177

F-NT2RM2001194//ESTs, Weakly similar to T28H10.2- [C.elegans] //2.4e-23:14  
9:93//Hs.10618:AI288739

F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959

F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:  
69//Hs.155291:D13630

F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.  
97:165:64//Hs.24279:AB018349

F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766

F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:

64//Hs.75889:U65928

F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066  
:321:61//Hs.132206:AF039694

F-NT2RM2001256

F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845

F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:  
182:65//Hs.75221:AF001601

F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615

F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.eleg  
ans]//5.2e-30:277:77//Hs.25347:AI138605

F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0  
.031:245:62//Hs.26915:AB008567

F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706

F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905

F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61/  
/Hs.82925:U70322

F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:  
U68382

F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378

F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e  
-97:453:99//Hs.155218:AJ007509

F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X  
57303

F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328  
:60//Hs.68900:AF016903

F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969

F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459

F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262

F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein aut

oantigen SS-A/Ro)//6.9e-28:582:64//Hs.1042:M62800  
 F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:5  
 7:89//Hs.114722:AA448077  
 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65/  
 /Hs.32168:AB007902  
 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729  
 F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//  
 Hs.76272:S66431  
 F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61  
 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073  
 F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918  
 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.  
 0e-154:740:98//Hs.15832:AB014518  
 F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952  
 F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [B  
 os taurus]//3.5e-13:94:92//Hs.22142:AA814725  
 F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61  
 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073  
 F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301  
 F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287  
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP)  
 mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195  
 F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH  
 6 [H.sapiens]//1.1e-136:671:97//Hs.27721:U17907  
 F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1  
 e-25:352:70//Hs.101414:AB011129  
 F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356  
 F-NT2RM2001675  
 F-NT2RM2001681//ESTs//0.16:197:63//Hs.20585:R10305

F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211  
 F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216  
 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//  
 5.8e-16:144:84//Hs.14671:T79937  
 F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415  
 F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817  
 F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein ( TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826  
 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788  
 F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650  
 F-NT2RM2001718  
 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//  
 Hs.12457:AF052123  
 F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0  
 e-112:530:98//Hs.129937:AB007931  
 F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.  
 95:269:58//Hs.129952:AB011132  
 F-NT2RM2001743  
 F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:A  
 B011399  
 F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61  
 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073  
 F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:AI222742  
 F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669:71//Hs.2479:  
 X78933  
 F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698  
 F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:AI193595  
 F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730)  
 containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770



F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763

F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:U29175

F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195

F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341

F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068

F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691

F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759

F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:86//Hs.113283:AF018080

F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567

F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421:66//Hs.8763:W30741

F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723

F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198:AB014610

F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892

F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937:AB007931

F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:U52840

F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U66688

F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//  
 2.2e-139:653:98//Hs.21811:AF091080  
 F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392  
 F-NT2RM2001982  
 F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds  
 //1.2e-21:123:98//Hs.6454:AF089816  
 F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.1041  
 35:AJ006778  
 F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538  
 F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:2  
 71:60//Hs.63888:AA203398  
 F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5  
 e-37:509:65//Hs.6214:AB018274  
 F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:4  
 29:58//Hs.79090:D89729  
 F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822  
 :73//Hs.1674:M90516  
 F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427  
 F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154  
 F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377  
 F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.896  
 31:U48508  
 F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partia  
 l//2.5e-165:776:98//Hs.99423:AJ010840  
 F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (G  
 AC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435  
 F-NT2RM2002128  
 F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274  
 F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, c

omplete cds//1.4e-144:800:92//Hs.20815:AF084928  
 F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7  
 e-165:787:97//Hs.11147:AB007936  
 F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palm  
 aris et plantaris)//0.064:291:61//Hs.99936:X14487  
 F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59  
 //Hs.148027:X63563  
 F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074  
 F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464  
 F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674  
 F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI038511  
 F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product is rel  
 ated to human RNA helicase A. [H.sapiens]//1.6e-30:369:70//Hs.114623:AI2  
 04280  
 F-NT2RM4000086  
 F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (Z  
 NF210) mRNA, complete cds//1.3e-24:345:69//Hs.13128:AF060865  
 F-NT2RM4000139  
 F-NT2RM4000155  
 F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632  
 F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, c  
 omplete cds//9.8e-30:676:61//Hs.159228:AF041853  
 F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044  
 F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190  
 F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744  
 F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//0.13:322:61//Hs.145088:AI221147  
 F-NT2RM4000200  
 F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.002

7:424:60//Hs.91400:AB006626

F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.

4e-184:856:98//Hs.111138:AB018255

F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013  
:358:60//Hs.75055:M93651

F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.  
65:572:60//Hs.47061:AF045458

F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582

F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439

F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccharomyce  
s pombe] //1.1e-16:112:92//Hs.93841:AA442297

F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, comp  
lete cds//1.8e-48:229:83//Hs.46328:D87942

F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, comp  
lete cds//2.5e-154:609:93//Hs.31305:M99438

F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds/  
/0.070:460:59//Hs.5372:AB000712

F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707

F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyces cer  
evisiae] //2.7e-83:432:95//Hs.12796:W27884

F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:  
68//Hs.155291:D13630

F-NT2RM4000354//ESTs, Weakly similar to lethal(2)denticleless [D.melanog  
aster] //0.0078:55:92//Hs.59075:AI023761

F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI418425

F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3  
e-135:628:99//Hs.8152:AB014542

F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745

F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25.

Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:843:68//Hs.23796:AL022718

F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029

F-NT2RM4000414//Homo sapiens XYLb mRNA for xylulokinase, complete cds//4.9e-17:114:94//Hs.137580:AB015046

F-NT2RM4000421

F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432:74//Hs.154872:AB011166

F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543:58//Hs.2175:M59820

F-NT2RM4000457

F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178:63//Hs.66369:U95040

F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:AI280004

F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632

F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915

F-NT2RM4000514

F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409

F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:AI221305

F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756:96//Hs.125870:AI364967

F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:H78987

F-NT2RM4000534

F-NT2RM4000585

F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593:62//Hs.7764:AB007938

F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans] //3.1e-104:532:96//Hs.6092:T75227

F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305:68//Hs.40100:AB002390

F-NT2RM4000611//EST//0.76:268:58//Hs.150031:AI292068

F-NT2RM4000616

F-NT2RM4000674

F-NT2RM4000689

F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529

F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744:77//Hs.42400:AF022789

F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus] //2.6e-163:771:97//Hs.6823:W18181

F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:M84605

F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743:98//Hs.137168:AB018303

F-NT2RM4000741

F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus] //1.1e-75:388:96//Hs.112361:R99396

F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:H67815

F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731

F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173:810:98//Hs.18586:AB007920

F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186

F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:98//Hs.25817:AC005306

F-NT2RM4000795//ESTs, Highly similar to LIVER CARBOXYLESTERASE PRECURSO

R [Homo sapiens] //6.7e-19:160:80//Hs.124902:AI337820  
 F-NT2RM4000796//Human K+ channel subunit gene, complete cds//0.96:292:62  
 //Hs.124212:M64676  
 F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301  
 F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subu  
 nit (SNAP190) mRNA, complete cds//0.052:238:64//Hs.113265:AF032387  
 F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H16568  
 F-NT2RM4000833  
 F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374:61//  
 Hs.7841:AB002322  
 F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934  
 F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN  
 SUBSTRATE 2 [Homo sapiens] //4.4e-29:164:95//Hs.115095:AI392943  
 F-NT2RM4000887  
 F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyr  
 ophosphorylase, complete cds//6.8e-22:407:64//Hs.21293:AB011004  
 F-NT2RM4000950  
 F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546  
 F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77  
 //Hs.7289:AB007875  
 F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381:67//Hs.2481:X  
 78926  
 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6  
 e-171:803:98//Hs.19542:AB018272  
 F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1  
 e-126:584:99//Hs.15711:AB014539  
 F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.  
 8e-05:469:58//Hs.5333:AB018254  
 F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus] //7

.0e-56:340:92//Hs.87310:AI247543  
 F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM  
 " PRECURSOR//0.79:142:69//Hs.77424:M63835  
 F-NT2RM4001084  
 F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62  
 //Hs.108947:D30758  
 F-NT2RM4001116  
 F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:  
 61//Hs.134989:L12701  
 F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730  
 F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:AI004145  
 F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351  
 F-NT2RM4001187  
 F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220  
 F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799:69//Hs.2479:  
 X78933  
 F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete c  
 ds//1.4e-153:707:99//Hs.14934:AF004828  
 F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEI  
 N ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]//0.19:291:62//Hs.31  
 582:AA877205  
 F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, c  
 omplete cds//7.0e-63:715:70//Hs.104925:AF059611  
 F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog [C  
 .elegans]//1.1e-67:208:96//Hs.26676:AA033997  
 F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.  
 0019:435:59//Hs.6360:AB007950  
 F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:  
 59//Hs.26971:AC003003



F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-7  
9:474:89//Hs.32971:Z46973

F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335

F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:  
66//Hs.87435:D89016

F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AI418988

F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEI  
N IN PMI40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0096:284  
:58//Hs.120997:R56714

F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat reg  
ion of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.7e-52:252:100//Hs  
.15301:AA167818

F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI277656

F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-  
169:790:98//Hs.5151:AF098799

F-NT2RM4001384

F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575

F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64/  
/Hs.105052:AB000520

F-NT2RM4001412

F-NT2RM4001414//ESTs, Moderately similar to F18547\_1 [H.sapiens]//5.2e-1  
8:133:87//Hs.28209:AI073817

F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:7  
0//Hs.154326:D42087

F-NT2RM4001444

F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658

F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914

F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sa  
piens]//1.1e-71:313:99//Hs.163754:AA587784

F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:AB014585

F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619

F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae] //1.3e-114:536:99//Hs.88820:AA456247

F-NT2RM4001557

F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487

F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453

F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859

F-NT2RM4001582

F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566

F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:AB011094

F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus] //2.3e-72:387:95//Hs.114722:AA448077

F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:AB018334

F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans] //8.6e-05:91:79//Hs.24647:W19739

F-NT2RM4001629//ESTs, Moderately similar to 55-KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens] //0.0042:153:68//Hs.114832:AI147946

F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320

F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323

F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638

F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384

F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957

F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905

F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903

F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318

F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306

F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719

F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:X97630

F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:AB018270

F-NT2RM4001783//ESTs, Weakly similar to T12D8.i [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677

F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NA P1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105

F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547

F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712

F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:AI379442

F-NT2RM4001828//Zinc finger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687

F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824

F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204

F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814

F-NT2RM4001856

F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator

T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250

F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.

3e-150:704:98//Hs.61628:Y17711

F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:6

6//Hs.7938:D86984

F-NT2RM4001880

F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212

F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:AI312633

F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, part

ial cds//0.98:359:57//Hs.155356:AJ224875

F-NT2RM4001938

F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-1

72:808:98//Hs.118631:AF098162

F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:8

3//Hs.154326:D42087

F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel.

[H.sapiens] //1.8e-65:337:96//Hs.130135:AA905493

F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862

F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.

2e-63:527:76//Hs.159277:AB018341

F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082

F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.7

3:181:65//Hs.11147:AB007936

F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271

F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601

F-NT2RM4002034

F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048

F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912

F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540

F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus] //7.0e-94:396:94//Hs.59346:AI126802

F-NT2RM4002063

F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309

F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040

F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302

F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.122967:AF059569

F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products} //9.2e-34:532:65//Hs.146459:X66975

F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743

F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542

F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877

F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158

F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens] //1.6e-135:646:97//Hs.104650:AI037879

F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535

F-NT2RM4002174

F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L2199

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F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//  
7.3e-11:454:60//Hs.32981:U38276

F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454

F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.5  
2:313:61//Hs.118087:AB011182

F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUN  
D [*Drosophila melanogaster*] //8.4e-125:588:98//Hs.23900:U82984

F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966

F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764

F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57  
//Hs.77783:AF014118

F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180

F-NT2RM4002281

F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979

F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:  
72//Hs.31463:D87457

F-NT2RM4002301

F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331

F-NT2RM4002339

F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454

F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.  
1e-151:708:98//Hs.26163:AB014549

F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0  
040:303:63//Hs.23741:AB018263

F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293

F-NT2RM4002390

F-NT2RM4002398

F-NT2RM4002409

F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans] //1.1e-55:282:96//Hs.26676:AA033997

F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:AF052151

F-NT2RM4002452

F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:81//Hs.115263:D30783

F-NT2RM4002460//EST//1.0:142:65//Hs.145370:AI252780

F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777:98//Hs.8765:AF083255

F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:97//Hs.94781:AB014591

F-NT2RM4002493

F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347

F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219

F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290:60//Hs.154968:U02020

F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075

F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AII/AVP mRNA, complete cds//1.0:100:70//Hs.159483:AF054176

F-NT2RM4002558//Homo sapiens amphipysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004

F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:D84273

F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans] //3.3e-88:484:93//Hs.105837:AA536054

F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylgl

alactosaminyltransferase [H.sapiens] //0.059:121:70//Hs.155413:AA429394  
 F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151  
 F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499:59//Hs.79357:D78275  
 F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402  
 F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587  
 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:AJ012449  
 F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907  
 F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647  
 F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834  
 F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792:AF044924  
 F-NT2RP1000111  
 F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699  
 F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:AI084025  
 F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens] //1.4e-71:382:94//Hs.127842:W38901  
 F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90//Hs.3760:AF011792  
 F-NT2RP1000170//EST//0.68:130:63//Hs.146994:AI184430  
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535  
 F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499  
 F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703  
 F-NT2RP1000243



F-NT2RP1000259

F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.4214:AF067730

F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661

F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551

F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231

F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204

F-NT2RP1000357

F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807

F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:86//Hs.77864:AB014538

F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96//Hs.120360:AF064594

F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031

F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:98//Hs.21862:AB011159

F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//7.3e-177:857:97//Hs.6823:W18181

F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.46:222:60//Hs.89230:AF031815

F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603

F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862

F-NT2RP1000460

F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, gen

omic sequence//3.7e-134:665:96//Hs.143187:AC002985  
 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs.159154:U47634  
 F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102  
 F-NT2RP1000493  
 F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977  
 F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992  
 F-NT2RP1000547//H.sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098  
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.104105:AF017418  
 F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213  
 F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385  
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770  
 F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.152936:D63475  
 F-NT2RP1000630  
 F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:U24576  
 F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553  
 F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:AI141736  
 F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148  
 F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.

0e-33:278:78//Hs.58167:D30612  
 F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens] //6.2e-40:297:84//Hs.18122:AI338045  
 F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644  
 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434  
 F-NT2RP1000746  
 F-NT2RP1000767  
 F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023  
 F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401  
 F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//2.7e-23:147:91//Hs.102336:Z83838  
 F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424:96//Hs.18953:AF067223  
 F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332903  
 F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI267990  
 F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI288838  
 F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875  
 F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023  
 F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094  
 F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218683  
 F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:AI248847  
 F-NT2RP1000916//ESTs, Weakly similar to coded for by C. elegans cDNA cm04e9 [C.elegans] //2.2e-27:159:94//Hs.122153:AA780270

F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U  
76248

F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400

F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbCH5B (UBCH5B) mR  
NA, complete cds//2.7e-26:185:87//Hs.108332:U39317

F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.1  
54276:AB002803

F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847

F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M1788  
5

F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858

F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//H  
s.82837:L13435

F-NT2RP1001011

F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163

F-NT2RP1001014

F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M6  
1764

F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901

F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531

F-NT2RP1001080//Homo sapiens forkhead protein (FKHRL1) mRNA, complete cd  
s//0.57:215:64//Hs.14845:AF032886

F-NT2RP1001113//ESTs, Weakly similar to coded for by C. elegans cDNA CEE  
SB82F [C.elegans]//1.4e-65:293:95//Hs.32751:H38087

F-NT2RP1001173

F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1  
e-26:259:74//Hs.75258:AF054174

F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524

F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150  
F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.25195:U81523  
F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094  
F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:AJ002231  
F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724  
F-NT2RP1001294  
F-NT2RP1001302  
F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341  
F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815  
F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770  
F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]//6.8e-101:480:94//Hs.75017:AA166853  
F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859  
F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673  
F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081  
F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700  
F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700  
F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149  
F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104  
F-NT2RP1001466  
F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742  
F-NT2RP1001482

F-NT2RP1001494

F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400

F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:  
254:64//Hs.75814:AB000277

F-NT2RP1001569

F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds  
//2.5e-41:496:74//Hs.12956:U90913

F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420

F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//  
4.7e-137:685:96//Hs.93677:AF091081

F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C.elegans]//8.2e-47:30  
0:89//Hs.6473:AA853955

F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:6  
8//Hs.40100:AB002390

F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:6  
6//Hs.70617:D31763

F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO  
MOLOG [Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359

F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1  
e-78:383:97//Hs.8309:AB018290

F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homol  
og (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749

F-NT2RP2000054//HOMEBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:  
L20433

F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase  
epsilon//1.2e-27:146:100//Hs.155991:X54134

F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25.  
Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (1

ymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022718

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609

F-NT2RP2000076//H.sapiens mRNA for TFIIA//0.00023:356:62//Hs.121686:D14887

F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078

F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338

F-NT2RP2000091

F-NT2RP2000097

F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963

F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390

F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-15:551:97//Hs.17706:AB018356

F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670

F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177

F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195

F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.152936:D63475

F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910

F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291

F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190  
 F-NT2RP2000173  
 F-NT2RP2000175  
 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protei  
 n 4, complete cds//0.0018:324:58//Hs.100058:AB006713  
 F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233  
 :90//Hs.56750:AI148761  
 F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050  
 F-NT2RP2000208  
 F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related prote  
 in 105, complete cds//0.0071:243:61//Hs.143641:AB009462  
 F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990  
 F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:34  
 2:59//Hs.8546:U97669  
 F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//  
 Hs.47822:AB002378  
 F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719  
 F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)  
 //0.51:227:60//Hs.30223:X90846  
 F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691  
 F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011  
 F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599  
 F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910  
 F-NT2RP2000288  
 F-NT2RP2000289  
 F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, com  
 plete cds//4.2e-60:744:70//Hs.37138:U35376  
 F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:AI123467  
 F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA



, complete cds//4.3e-13:140:80//Hs.58218:U82381  
 F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:AI417006  
 F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:AI332905  
 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66  
 //Hs.101642:X60673  
 F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:1  
 26:69//Hs.153706:AF026547  
 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA,  
 complete cds//1.2e-130:627:97//Hs.76556:U83981  
 F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.5  
 6:464:57//Hs.12259:AB014530  
 F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047  
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67  
 :375:93//Hs.808:L28010  
 F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapie  
 ns] //3.9e-75:413:92//Hs.36779:AA626790  
 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,  
 complete cds//6.7e-128:609:96//Hs.5819:AF102265  
 F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381  
 F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402:AI393918  
 F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e-22:158:87//Hs.154655:  
 Z68747  
 F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293  
 F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702  
 F-NT2RP2000510  
 F-NT2RP2000516  
 F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B MRNA EDITING P  
 ROTEIN [Rattus norvegicus] //3.2e-15:167:75//Hs.10984:AA806768  
 F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6

e-38:196:98//Hs.14409:AB011144  
 F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//1.0:242:57//Hs.114001:Z20656  
 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732:97//Hs.7314:AB014514  
 F-NT2RP2000644//ESTs//0.035:276:60//Hs.43660:N33174  
 F-NT2RP2000656  
 F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602  
 F-NT2RP2000668  
 F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:AI093453  
 F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [*Caenorhabditis elegans*]//2.4e-31:233:78//Hs.114905:AA088442  
 F-NT2RP2000710  
 F-NT2RP2000715  
 F-NT2RP2000731  
 F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA573242  
 F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [*Saccharomyces cerevisiae*]//1.6e-74:445:89//Hs.21421:AA911739  
 F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101  
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:58//Hs.159275:AF030880  
 F-NT2RP2000814  
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182  
 F-NT2RP2000819  
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:70//Hs.20695:AB002292  
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, compl

ete cds//9.5e-29:167:94//Hs.75794:U80811

F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:AI336850

F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2  
F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]//6.4e-34:207:92//Hs.1  
35235:AI081880

F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.  
7e-142:732:94//Hs.3615:AB018284

F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase  
kinase 5 [H.sapiens]//0.50:189:65//Hs.46146:AA418097

F-NT2RP2000931//MATRIN 3//1.1e-130:610:98//Hs.78825:AB018266

F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326:9  
7//Hs.15144:AC005014

F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408

F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.  
9e-113:533:98//Hs.19822:AB018298

F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494

F-NT2RP2000970

F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN  
SIS2-MTD1 INTERGENIC REGION [Saccharomyces cerevisiae]//7.3e-76:385:96//  
Hs.21875:AA243700

F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944

F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292

F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117

F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0488//1.0e-145:696:97//Hs.67619:AB007957

F-NT2RP2001065

F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//H  
s.3989:AB002313

F-NT2RP2001081

F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:AI356560

F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.  
.155464:AF088219

F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:  
63//Hs.80358:U52191

F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR  
ALPHA [Bos taurus]//6.4e-34:201:91//Hs.118470:AI336362

F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582

F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:AI091361

F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.  
4e-114:567:96//Hs.26247:AB007949

F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011

F-NT2RP2001196

F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598

F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.  
2685:Z50053

F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//  
Hs.69740:U09367

F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813

F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1  
e-108:514:97//Hs.7531:AB018353

F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277

F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:  
76//Hs.75848:U39412

F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287

F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387

F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs  
.76090:M80783

F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522

F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41883

F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:41  
8:91//Hs.107039:W27244

F-NT2RP2001378

F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:AI377558

F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155),  
complete sequence//0.28:225:62//Hs.159402:AC005609

F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767

F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088

F-NT2RP2001420

F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]  
//0.030:443:59//Hs.140506:AA308018

F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875

F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966

F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase acti  
vation protein, eta polypeptide//9.8e-56:603:72//Hs.75544:Z82248

F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218

F-NT2RP2001449

F-NT2RP2001450

F-NT2RP2001467

F-NT2RP2001506

F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409  
:98//Hs.156161:AI333779

F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARAL  
AR1//6.4e-138:657:97//Hs.4277:Y14494

F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134

F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3  
(XRCC3) mRNA, complete cds//5.2e-105:384:94//Hs.99742:AF035586

F-NT2RP2001560

F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0488//1.4e-124:590:98//Hs.67619:AB007957

F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:5  
21:60//Hs.75936:U28389

F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876

F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//  
Hs.82201:M55268

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3  
e-138:647:98//Hs.27197:AB018340

F-NT2RP2001613

F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI082229

F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA,  
complete cds//4.9e-124:604:96//Hs.58488:U97067

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD  
subunit brain-specific isoform mRNA, complete cds//1.3e-145:687:97//Hs.1  
59558:AF058718

F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328

F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58//Hs.96264:U72936

F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.0  
28:285:63//Hs.6162:AB018314

F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.  
7e-34:328:76//Hs.27621:U52840

F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091

F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.mu  
sculus]//1.0:173:62//Hs.107361:AI197870

F-NT2RP2001721

F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:  
57//Hs.8114:AF022991

F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate sy

nthetase, dimethylallyltranstransferase, geranyltranstransferase)//1.2e-19:151:86//Hs.77393:D14697

F-NT2RP2001762//Homo sapiens exonuclease 1a (EX01a) mRNA, complete cds//5.2e-34:191:96//Hs.47504:AF091754

F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180

F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI052250

F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610

F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443:AF027219

F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768

F-NT2RP2001883

F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR//3.0e-113:633:90//Hs.142189:M74161

F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650

F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//0.37:263:62//Hs.106377:H29757

F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI393754

F-NT2RP2001936

F-NT2RP2001943

F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797

F-NT2RP2001947

F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489

F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892

F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:AB011117

F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196

F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:AB018299

F-NT2RP2002032

F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI003543

F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336

F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509

F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284198

F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284

F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:66//Hs.44553:AF055634

F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241

F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183

F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014

F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI313156

F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533:97//Hs.155218:AJ007509

F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.122755:AF032986

F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286

F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:M83363

F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112

F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314

F-NT2RP2002185//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//6.8e-61:354:91//Hs.109966:C06057

F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7



e-37:194:97//Hs.91728:M58460

F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein  
PIASx-alpha mRNA, complete cds//6.8e-15:228:67//Hs.111323:AF077954

F-NT2RP2002208

F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628

F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394318

F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264  
:U70439

F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.7  
9:264:59//Hs.129748:AB011099

F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cd  
s//2.1e-51:315:89//Hs.150595:AF005418

F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//  
Hs.92137:M19720

F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//1.3e-3  
1:206:88//Hs.4029:Z78373

F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079

F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA,  
partial cds//5.0e-95:467:96//Hs.24812:AF069532

F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445

F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA  
, complete cds//1.3e-124:640:95//Hs.31034:AB015594

F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60/  
/Hs.75516:X54637

F-NT2RP2002373

F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant m  
RNA, complete cds//3.1e-139:673:97//Hs.109051:AF038958

F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U  
79289

F-NT2RP2002408//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74095:L20433

F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098

F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326

F-NT2RP2002442//ESTs, Weakly similar to similar to molybdoterin biosynthesis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA904265

F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs.1560:D42045

F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:AI139929

F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs.125856:AB005289

F-NT2RP2002498

F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs.102681:U95044

F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs.23255:AB018334

F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563:M28212

F-NT2RP2002537

F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096

F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979

F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs.159277:AB018341

F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309

F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs.23094:M19503

F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs.334:U02082

F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805

F-NT2RP2002621

F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs.155302:U57317

F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493

F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK 757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109857:AA088385

F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs.6336:AB014572

F-NT2RP2002727

F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217

F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297

F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs.87435:D89016

F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs.146395:AB002329

F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709

F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705

F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs.79706:U53204

F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407

F-NT2RP2002800

F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763

F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:AI382142

F-NT2RP2002862

F-NT2RP2002880

F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0  
:237:62//Hs.106487:AB014573

F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606

F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.116674:AF038392

F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:15  
8:65//Hs.108447:AJ000517

F-NT2RP2002939

F-NT2RP2002954

F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds//6.4e-21:135:91//Hs.108332:U39317

F-NT2RP2002979

F-NT2RP2002980

F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs.122967:AF059569

F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:AI004740

F-NT2RP2002993

F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs  
.155464:AF088219

F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741

F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019

F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190

F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs  
.153704:U11050

F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633

F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:AI291379

F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:556:57//Hs.155321:J03161

F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544

F-NT2RP2003137

F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.4  
0:227:61//Hs.105958:AB014520

F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete c  
ds//5.7e-113:581:93//Hs.9736:D67025

F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:AI424170

F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944

F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:  
79//Hs.153014:AB002353

F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:N91123

F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:AI393223

F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594

F-NT2RP2003228//CDC21, HOMOLOG//9.3e-138:726:93//Hs.154443:X74794

F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947

F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phos  
phate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//Hs.108966:U486  
96

F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear prot  
ein isoform mRNA, partial cds//0.52:200:62//Hs.102732:U88153

F-NT2RP2003265

F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]  
//5.8e-57:313:93//Hs.109966:C06057

F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9  
e-147:714:96//Hs.154919:AB014525

F-NT2RP2003280

F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.  
0097:243:65//Hs.21862:AB011159

F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:AI269334

F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds//2.0e-86:416:97//Hs.7943:AB006572

F-NT2RP2003297//EST//0.99:240:60//Hs.133228:AI052312

F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752

F-NT2RP2003308

F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:532:95//Hs.6092:T75227

F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:AI346765

F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963

F-NT2RP2003367//Human HsLIM15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108

F-NT2RP2003391

F-NT2RP2003393

F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023

F-NT2RP2003401

F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//3.7e-33:303:77//Hs.14038:R06800

F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893

F-NT2RP2003446//Prostaglandin receptor, epl subtype//0.81:273:61//Hs.159360:L22647

F-NT2RP2003456//EST//0.17:95:65//Hs.147190:AI193320

F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770

F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106

F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136

F-NT2RP2003506

F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.1071  
64:M96803

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:9  
4//Hs.78482:Y16270

F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian  
sarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783

F-NT2RP2003522//Zinc finger protein 148 (pHZ-52)//1.1e-17:512:60//Hs.112  
180:AF039019

F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765

F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010

F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:AI356513

F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein aut  
oantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800

F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3  
e-114:541:98//Hs.129937:AB007931

F-NT2RP2003581//EST//1.0:59:76//Hs.158575:AI368947

F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.eleg  
ans]//1.3e-63:224:95//Hs.34627:AA126463

F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA,  
complete cds//1.7e-124:585:98//Hs.58488:U97067

F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166

F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M972  
52

F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HP  
X42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006

F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:AI032875

F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247

F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61

//Hs.18366:L09561

F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44:269:91//Hs.139757:N95271

F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097

F-NT2RP2003713

F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180

F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879

F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme Ubch5C (UBCH5C) mRNA, complete cds//4.0e-55:584:71//Hs.118797:U39318

F-NT2RP2003751

F-NT2RP2003760

F-NT2RP2003764

F-NT2RP2003769

F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677

F-NT2RP2003777

F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63:356:92//Hs.16131:AA568689

F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955

F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742

F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368

F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425

F-NT2RP2003859

F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780

F-NT2RP2003885

F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emericella nidulans]//2.2e-113:632:92//Hs.50072:AI378221



F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H  
.sapiens] //1.0:146:67//Hs.156920:AA489296

F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease,  
complete cds//6.8e-30:165:96//Hs.35086:AB014458

F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.  
9e-116:610:94//Hs.7302:AB007916

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2  
e-161:783:96//Hs.7316:AB018347

F-NT2RP2003984

F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036

F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124  
:AF019369

F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo  
sapiens] //7.0e-104:556:93//Hs.111081:AI380378

F-NT2RP2004014

F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:8  
0//Hs.10116:AC004780

F-NT2RP2004042

F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete  
cds//0.80:292:61//Hs.1147:AF011573

F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942

F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2)  
mRNA, complete cds//0.15:199:60//Hs.104315:AF054828

F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:  
AJ007292

F-NT2RP2004142

F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872

F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.6  
9:176:63//Hs.78353:U88666

F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966  
 F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501  
 F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapie  
 ns] //1.7e-16:276:67//Hs.36779:AA626790  
 F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete  
 cds//1.0:124:69//Hs.155302:U57317  
 F-NT2RP2004196  
 F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756  
 F-NT2RP2004226//ESTs, Weakly similar to teg292 protein [M.musculus] //1.8  
 e-80:386:98//Hs.68791:AA527270  
 F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756  
 F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680  
 F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536  
 F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:5  
 9//Hs.129725:AF047487  
 F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.eleg  
 ans] //8.2e-51:474:74//Hs.108990:N25951  
 F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//  
 Hs.112432:AC005263  
 F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS  
 E BETA 3//0.35:157:67//Hs.37121:Z37544  
 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete c  
 ds//1.5e-151:735:97//Hs.61152:AF000416  
 F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735  
 F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510  
 F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632  
 F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202  
 F-NT2RP2004365  
 F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript

//0.60:295:57//Hs.39163:AF000986

F-NT2RP2004373

F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F0  
9G8.3 IN CHROMOSOME III [Caenorhabditis elegans] //3.3e-97:477:98//Hs.304  
90:AA146916

F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588

F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21//1.4e-174:875:  
95//Hs.152759:AC005164

F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans] //1.2e-92:51  
9:91//Hs.13275:AI341468

F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367

F-NT2RP2004412

F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944

F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687

F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TAS  
K) mRNA, complete cds//0.45:208:61//Hs.24040:AF006823

F-NT2RP2004490

F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203

F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA,  
complete cds//1.3e-29:270:79//Hs.73614:U83460

F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6  
e-139:687:96//Hs.129908:AB011163

F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891

F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-0  
6:291:61//Hs.132206:AF039694

F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs  
.155464:AF088219

F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.  
98:136:64//Hs.28020:AB018309

F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.  
0:104:68//Hs.125729:N99898

F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.  
.24756:U43895

F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens]//3.0e-59:273:93//Hs.12845:N28835

F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908

F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496  
:98//Hs.5198:AJ006291

F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2  
e-155:728:98//Hs.29956:AB007929

F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839

F-NT2RP2004681

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1  
e-61:327:94//Hs.154919:AB014525

F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942

F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780

F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.  
1e-118:582:96//Hs.4236:AB007947

F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242

F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183

F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE  
PAK [Rattus norvegicus]//3.7e-110:548:96//Hs.85768:W16504

F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA  
, complete cds//0.025:547:57//Hs.107474:AF045451

F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete  
cds//0.99:121:64//Hs.2864:L40157

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta s  
ubunit (SCS) mRNA, partial cds//4.9e-118:594:95//Hs.40820:AF058953

F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043  
F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:AF054179  
F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161  
F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258  
F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111  
F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144  
F-NT2RP2004936  
F-NT2RP2004959  
F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763  
F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478  
F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735  
F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927  
F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.41723:U37426  
F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478  
F-NT2RP2004999  
F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//Hs.124161:AF065164  
F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:AB014515  
F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200  
F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141

F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600  
 F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433  
 F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067  
 F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035  
 F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612  
 F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:AF055917  
 F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838  
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:98//Hs.22616:AB014564  
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs.100555:X98743  
 F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803  
 F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947  
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226:AF045583  
 F-NT2RP2005147  
 F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI357582  
 F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:AI357868  
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:96//Hs.155218:AJ007509  
 F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159  
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189

F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783  
F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264  
:U70439  
F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.  
56:114:68//Hs.154503:U36341  
F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete  
cds//1.2e-40:594:65//Hs.81452:AF030555  
F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI383932  
F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, com  
plete cds//2.3e-123:604:96//Hs.27007:AF060219  
F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.  
44766:AJ007590  
F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833  
F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6  
e-97:483:96//Hs.115763:AB014576  
F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete  
cds//2.6e-23:166:90//Hs.1569:U11701  
F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subu  
nit (SNAP190) mRNA, complete cds//0.016:353:62//Hs.113265:AF032387  
F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8  
e-30:456:66//Hs.44697:AB011138  
F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958  
F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA  
, complete cds//1.4e-100:489:96//Hs.107254:AC005943  
F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122  
F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, co  
mplete cds//0.87:244:59//Hs.113252:U80761  
F-NT2RP2005407  
F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.2

8:338:57//Hs.6189:AB011133  
 F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068  
 F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164  
 F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE  
 SUBUNIT B14.5B [Bos taurus]//8.5e-48:295:90//Hs.75017:AA166853  
 F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243  
 F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//0.032:1  
 76:64//Hs.16:D10656  
 F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:AI378412  
 F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds//9.  
 9e-48:432:77//Hs.15519:AB018315  
 F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573  
 F-NT2RP2005491  
 F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:AI084164  
 F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-48:621:6  
 8//Hs.6833:AB002324  
 F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete  
 cds//1.6e-63:503:78//Hs.7688:M64930  
 F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.56:13  
 9:66//Hs.8546:U97669  
 F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthe  
 tase), regulatory (30.8kD)//1.0:291:59//Hs.89709:L35546  
 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mR  
 NA, complete cds//1.2e-82:444:92//Hs.119023:AF092563  
 F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//2.  
 2e-19:112:99//Hs.6232:AB018307  
 F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1  
 [H.sapiens]//3.5e-50:366:83//Hs.61833:AA036735  
 F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//9.4e



-155:747:97//Hs.159597:AJ012449

F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.

9e-131:618:98//Hs.62515:AB007963

F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16  
C10.10 IN CHROMOSOME III [C.elegans]//2.5e-51:292:93//Hs.105684:H24407

F-NT2RP2005555//EST//0.046:308:57//Hs.145962:AI276822

F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:AI422839

F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436

F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:AI218627

F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071

F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:97  
//Hs.22396:AF062085

F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702

F-NT2RP2005635

F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905

F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:AI292145

F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:AI375440

F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.143065:M86  
917

F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-  
08:351:62//Hs.91400:AB006626

F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239

F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, co  
mplete cds//7.7e-96:462:98//Hs.25664:AF089814

F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702

F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79  
217:M77836

F-NT2RP2005694

F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) m

RNA, complete cds//0.15:496:55//Hs.79326:L76703  
 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1  
 e-126:599:97//Hs.61638:AB018342  
 F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527  
 F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//  
 Hs.69740:U09367  
 F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017  
 F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:AI334191  
 F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086  
 F-NT2RP2005741//Homo sapiens chondroadherin gene, 5' flanking region and/  
 /0.80:362:58//Hs.97220:U96769  
 F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688  
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, c  
 omplete cds//2.5e-23:134:96//Hs.159651:AF068868  
 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, comple  
 te cds//4.0e-102:486:98//Hs.26285:AF082516  
 F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425  
 :56//Hs.79768:D21853  
 F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23  
 205:X82895  
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79  
 217:M77836  
 F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//  
 1.7e-42:645:64//Hs.78769:Z50115  
 F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556  
 F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop  
 -helix protein//2.9e-06:201:67//Hs.34853:U28368  
 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820  
 F-NT2RP2005812

F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595

F-NT2RP2005835

F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA,  
complete cds//0.94:148:65//Hs.59829:AB014602

F-NT2RP2005853

F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA,  
partial cds//5.4e-176:829:98//Hs.50758:AF092564

F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567

F-NT2RP2005868

F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial  
cds//0.26:728:57//Hs.240:L16782

F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943

F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360

F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399

F-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//  
7.9e-90:326:98//Hs.156882:AA292186

F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770

F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339

F-NT2RP2006023

F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382

F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.5  
1:271:59//Hs.37035:U07664

F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093

F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58  
//Hs.57652:D87469

F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416

F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970

F-NT2RP2006100

F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135

F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349  
F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240  
F-NT2RP2006166  
F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73/  
/Hs.74368:X69910  
F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5  
e-114:567:96//Hs.109299:AB014554  
F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.  
0e-23:187:85//Hs.15519:AB018315  
F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503  
F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.15  
3910:X96484  
F-NT2RP2006237  
F-NT2RP2006238  
F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970  
F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//  
0.019:111:71//Hs.157199:X97630  
F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding mo  
tif, complete cds//2.4e-05:388:60//Hs.75111:D87258  
F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:  
598:97//Hs.3404:AF035262  
F-NT2RP2006320//ESTs, Moderately similar to maternal transcript Maid [M.  
musculus]//1.9e-29:151:100//Hs.36794:AI038407  
F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371  
F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:  
70//Hs.87202:D82344  
F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0  
.11:43:100//Hs.6892:AF076974  
F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1

e-05:233:65//Hs.37656:AB011174  
 F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501  
 F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341  
 F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.95838:AF059734  
 F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934  
 F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509  
 F-NT2RP2006456  
 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//1.1e-149:545:98//Hs.72160:AJ006266  
 F-NT2RP2006467  
 F-NT2RP2006472  
 F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048  
 F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134  
 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966  
 F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.73864:U22029  
 F-NT2RP2006573  
 F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223  
 F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180  
 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-137:637:98//Hs.6764:AJ011972  
 F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:AF000560  
 F-NT2RP3000047  
 F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.37138:U35376  
 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961

F-NT2RP3000068

F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769

F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353  
:78//Hs.108287:L27670

F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//H  
s.80741:X14608

F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140

F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595

F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:  
438:100//Hs.8173:AC005189

F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9  
e-182:849:98//Hs.13273:AB011164

F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1  
e-20:133:94//Hs.23094:M19503

F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0492//6.6e-08:152:71//Hs.127338:AB007961

F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779

F-NT2RP3000207

F-NT2RP3000220

F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete  
cds//6.6e-20:509:58//Hs.122967:AF059569

F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740

F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691  
:86//Hs.75863:D86972

F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733

F-NT2RP3000252

F-NT2RP3000255

F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568

F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, comp

lete cds//1.7e-13:214:67//Hs.80261:L43821  
 F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863  
 F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear prot  
 ein isoform mRNA, partial cds//0.0088:236:63//Hs.102732:U88153  
 F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:AI091242  
 F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase  
 kinase 5 [H.sapiens] //0.57:189:65//Hs.46146:AA418097  
 F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:7  
 8//Hs.40100:AB002390  
 F-NT2RP3000348  
 F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.  
 78582:X80754  
 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66  
 //Hs.101642:X60673  
 F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921  
 F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Ly  
 mnaea stagnalis] //4.0e-116:596:95//Hs.21094:AI337016  
 F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639  
 F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873  
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cd  
 s//1.6e-175:841:97//Hs.28307:AF071185  
 F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7  
 e-33:610:65//Hs.23094:M19503  
 F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948  
 F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487  
 F-NT2RP3000441  
 F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:AI051562  
 F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.  
 75562:U48705

F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068  
 F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:AI289822  
 F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058  
 F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667  
 F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379  
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:  
 63//Hs.79347:D86966  
 F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308  
 F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412  
 F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404  
 F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723  
 F-NT2RP3000578  
 F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277  
 F-NT2RP3000584  
 F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904  
 F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:5  
 7//Hs.77234:AB001914  
 F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811  
 F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:35  
 5:92//Hs.114622:AA693492  
 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:5  
 9//Hs.79170:D86980  
 F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:AI421203  
 F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683  
 F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162  
 F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:AI017333  
 F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904  
 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs  
 .155464:AF088219



F-NT2RP3000661

F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.13063:AF017789

F-NT2RP3000685

F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001

F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884

F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854

F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:AI369426

F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765

F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245:91//Hs.2427:D89937

F-NT2RP3000815

F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132

F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700

F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN A P47 HOMOLOG 2 [H.sapiens]//1.1e-71:363:96//Hs.23803:AA126476

F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012

F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593:68//Hs.157199:X97630

F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520

F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:86//Hs.155464:AF088219

F-NT2RP3000852

F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699918

F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476

F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766:60//Hs.15432:U53445

F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60

//Hs.79706:U53204

F-NT2RP3000875

F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101

F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI348374

F-NT2RP3000917

F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340:60//Hs.109895:X68277

F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X844

07

F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:AI204212

F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411

F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N92198

F-NT2RP3001007

F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//2.9e-121:588:98//Hs.128781:AA160707

F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282:97//Hs.30303:AI244662

F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534:74//Hs.27007:AF060219

F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474:60//Hs.21264:AB018325

F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP ...)//4.4e-16:428:60//Hs.155481:AJ006470

F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:64//Hs.82292:D86969

F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:AI337050

F-NT2RP3001111

F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088

F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023

F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779

F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:61//Hs.12107:AF042384

F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687:75//Hs.69740:U09367

F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:60//Hs.94790:AB018318

F-NT2RP3001133//Homeo box A4//0.00011:484:59//Hs.77637:M74297

F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:98//Hs.5378:AB018305

F-NT2RP3001147

F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605

F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891:98//Hs.72160:AJ006266

F-NT2RP3001176

F-NT2RP3001214//EST//0.88:218:60//Hs.161147:AI417859

F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W19981

F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512:95//Hs.103816:AA130866

F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010

F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756

F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:L06237

F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132

F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:293:60//Hs.32934:U27109

F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:64//Hs.107809:AB018269

F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.2e-42:454:72//Hs.41728:L75847

F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566  
 F-NT2RP3001274  
 F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811  
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:69//Hs.31463:D87457  
 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437:U44060  
 F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.012:522:56//Hs.904:U84010  
 F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731  
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966  
 F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:AB007920  
 F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.00019:473:61//Hs.124161:AF065164  
 F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER I SOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831  
 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487  
 F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022  
 F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451  
 F-NT2RP3001384//Homa sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332  
 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595  
 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783  
 F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB)

domain polypeptide)//1.0e-05:189:66//Hs.41728:L75847  
 F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CT  
 P) mRNA, 3' end//0.77:132:66//Hs.111024:L77567  
 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658  
 F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047  
 F-NT2RP3001426  
 F-NT2RP3001427  
 F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:  
 431:91//Hs.85844:X66397  
 F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNIN  
 G ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393  
 F-NT2RP3001447  
 F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.  
 89631:U48508  
 F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212  
 F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323  
 F-NT2RP3001459  
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, compl  
 ete cds//4.2e-10:168:70//Hs.32317:AF072836  
 F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877  
 F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231  
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (T  
 RC8) mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801  
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA,  
 complete cds//9.4e-139:743:91//Hs.85283:U36500  
 F-NT2RP3001529//ESTs, Moderately similar to topoisomerase I C-terminal f  
 ragment [H.sapiens]//0.28:224:65//Hs.105912:AI431328  
 F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074  
 F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.14

7918:U38291

F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:42  
6:59//Hs.162:X16302

F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11  
(Gq class)//0.049:185:65//Hs.1686:M69013

F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.  
6e-51:345:82//Hs.144563:AF057280

F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688

F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349

F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435

F-NT2RP3001629

F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:2  
76:97//Hs.9899:AF099149

F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173

F-NT2RP3001646

F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e  
-172:816:98//Hs.159597:AJ012449

F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027

F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseud  
omonas fluorescens]//9.0e-53:375:85//Hs.41127:AA555184

F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65/  
/Hs.79077:D87071

F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK  
757.1 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-111:518:99//Hs.20  
364:AI420022

F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63  
//Hs.7486:D83198

F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329

F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219

F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRE  
CURSOR [D.melanogaster] //1.4e-31:191:94//Hs.131279:AA486291

F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41  
:259:59//Hs.58435:AF001862

F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PR  
ECURSOR [Mus musculus] //7.6e-159:747:98//Hs.6823:W18181

F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein m  
RNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177

F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK  
686.3 IN CHROMOSOME III [Caenorhabditis elegans] //3.5e-116:554:98//Hs.14  
4332:AA046836

F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:  
78//Hs.90998:D50918

F-NT2RP3001739

F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.  
116549:AL009172

F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator  
T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.22138:U49250

F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2  
.4e-47:725:64//Hs.41688:U27193

F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mR  
NA, complete cds//0.42:198:61//Hs.57783:U78525

F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1  
e-153:710:98//Hs.28169:AB007928

F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.  
79024:L03532

F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361

F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L4116

F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379  
:58//Hs.32950:X82634

F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729

F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.  
8e-35:481:67//Hs.158225:U68727

F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706

F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.elegans  
]//2.9e-94:452:98//Hs.54952:AA872675

F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6  
139:AL022326

F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896

F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185

F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247

F-NT2RP3001931

F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022  
:268:61//Hs.106070:U22398

F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.  
8e-167:815:96//Hs.15869:AB014575

F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335

F-NT2RP3001969

F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180

F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs  
.155464:AF088219

F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.7508  
7:X86779

F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946

F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821

F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67/  
/Hs.147189:D88153



F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus] //3.8e-48:353:81//Hs.127507:AA993745

F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens] //3.0e-25:212:83//Hs.71622:AA195155

F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens] //4.2e-82:407:97//Hs.131888:AI091806

F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503

F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710

F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//0.91:194:65//Hs.1298:J03779

F-NT2RP3002081

F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.073:297:61//Hs.102732:U88153

F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256

F-NT2RP3002108

F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018

F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260

F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009

F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644

F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985

F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus] //3.0e-61:340:93//Hs.11379:AA594140

F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046

F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1  
098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141  
429:AA631915

F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA306435

F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (card  
iomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656

F-NT2RP3002248

F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261

F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complet  
e cds//0.42:189:62//Hs.110637:AC004080

F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139

F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386

F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//  
1.3e-05:496:60//Hs.21537:X80910

F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871

F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:  
462:56//Hs.143624:AF033383

F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1  
.6e-65:588:75//Hs.154672:X16396

F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A)  
gene//4.2e-166:770:98//Hs.6483:Y16355

F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5  
e-161:911:89//Hs.2397:Z70200

F-NT2RP3002399

F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233  
:94//Hs.22880:AA056274

F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9  
e-140:649:99//Hs.12707:AB014578

F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:AI291310  
 F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108  
 F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0  
 :173:61//Hs.81234:AB007935  
 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, com  
 plete cds//4.4e-146:763:93//Hs.57738:U35246  
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9  
 e-180:833:98//Hs.19542:AB018272  
 F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sap  
 iens] //1.3e-42:510:70//Hs.96759:AA469984  
 F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X787  
 06  
 F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054  
 F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919  
 F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.  
 89631:U48508  
 F-NT2RP3002603  
 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:6  
 1//Hs.3845:AB014888  
 F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.  
 121287:AF029900  
 F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP  
 )//2.6e-13:441:63//Hs.155481:AJ006470  
 F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, compl  
 ete cds//1.7e-05:615:58//Hs.151518:U38847  
 F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308  
 F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo  
 sapiens] //4.1e-38:493:70//Hs.41086:AI337400  
 F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI421991

F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:29  
4:100//Hs.128750:AI367584

F-NT2RP3002687

F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI352200

F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI393657

F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279514

F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291

F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6)  
gene, partial cds//0.91:161:62//Hs.129736:AF040753

F-NT2RP3002785

F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713

F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:42  
3:93//Hs.41068:AA844350

F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete c  
ds//2.2e-55:615:70//Hs.105940:AF004715

F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070

F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582

F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88  
//Hs.123090:AB001895

F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040

F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8  
e-181:853:98//Hs.6162:AB018314

F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765

F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila  
melanogaster]//1.4e-133:645:97//Hs.3826:U69560

F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.  
2e-13:594:57//Hs.74599:AB011160

F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.  
76:412:57//Hs.21198:AB018262

F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870

F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997

F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI287703

F-NT2RP3002985//Human TFIIB related factor hBRF (HBRF) mRNA, complete cds//0.071:550:58//Hs.32935:U28838

F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308

F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083

F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446

F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749

F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609

F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928

F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079

F-NT2RP3003078

F-NT2RP3003101

F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//0.98:88:68//Hs.99715:AA292700

F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740

F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.101299:AF017061

F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975

F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:63//Hs.118397:AF053944

F-NT2RP3003150

F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.37138:U35376

F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.0

45:410:59//Hs.6150:AB011093

F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:  
X78933

F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211

F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854

F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308

F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325

F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525

F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//  
6.0e-55:587:70//Hs.109606:D44497

F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds/  
/1.2e-129:617:98//Hs.155223:AF055460

F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200

F-NT2RP3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, c  
omplete cds//0.069:382:59//Hs.620:M69225

F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0  
.98:261:59//Hs.30792:AF044924

F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:  
694:93//Hs.11702:L36983

F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.757  
89:D87953

F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947

F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1  
e-91:681:80//Hs.23094:M19503

F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947

F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058

F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200

F-NT2RP3003330

F-NT2RP3003344

F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase  
//1.2e-42:644:66//Hs.2638:Z28339

F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L788  
33

F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//  
Hs.148090:D83542

F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791

F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:9  
6//Hs.21263:H16363

F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850

F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA,  
complete cds//3.2e-22:430:63//Hs.113272:U90653

F-NT2RP3003411//Human metallothionein-Ie gene (hMT-Ie)//0.99:116:62//Hs.  
74170:M10942

F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830

F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:  
243:61//Hs.62:M93425

F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete c  
ds//1.7e-182:853:98//Hs.14934:AF004828

F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2  
e-175:826:98//Hs.26450:AB018268

F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98  
330

F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302

F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete  
cds//0.64:626:58//Hs.150828:AF038169

F-NT2RP3003552

F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:AI418322

F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365

F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311  
 F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247  
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56  
 741  
 F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:56  
 4:61//Hs.104:D14012  
 F-NT2RP3003625  
 F-NT2RP3003656  
 F-NT2RP3003659  
 F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586  
 F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184  
 F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mR  
 NA, complete cds//0.013:190:63//Hs.44585:U58334  
 F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69  
 :246:62//Hs.118463:AF055000  
 F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848  
 F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61  
 //Hs.48998:AB007865  
 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.  
 4e-150:700:98//Hs.48513:AB018300  
 F-NT2RP3003746  
 F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230  
 F-NT2RP3003799  
 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene ho  
 molog//4.7e-41:432:73//Hs.1422:M19722  
 F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (card  
 iomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656  
 F-NT2RP3003809//Human transcription factor, forkhead related activator 4  
 (FREAC-4) mRNA, complete cds//5.1e-07:624:59//Hs.96028:AF042832



F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171:63//Hs.102877:U41315

F-NT2RP3003825

F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:AI346481

F-NT2RP3003831

F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300:AF070611

F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:M73780

F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268

F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738:AB018343

F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243:90//Hs.124832:AA846576

F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//1.1e-107:499:99//Hs.105794:AA701659

F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49:404:77//Hs.9006:AF057358

F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396

F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006

F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433:58//Hs.93909:AF042498

F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H. sapiens]//2.8e-127:617:97//Hs.142151:AA984061

F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs.155302:U57317

F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234

F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:

67//Hs.26441:AB002317

F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875

F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520:90//Hs.100007:X76091

F-NT2RP3004093

F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258

F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390

F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCO F7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:AI096509

F-NT2RP3004145

F-NT2RP3004148

F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:AF032900

F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706

F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:62//Hs.101047:M31523

F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835

F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361

F-NT2RP3004242

F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240

F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:AI149140

F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067

F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.158471:AF088982

F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:  
597:61//Hs.19261:AF007871

F-NT2RP3004332

F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285

F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426

F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999

F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1  
098.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141  
429:AA631915

F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen a  
lpha chain 1(V) chain [C.elegans]//4.3e-125:608:98//Hs.128781:AA160707

F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein  
1//2.3e-141:804:90//Hs.123122:X97249

F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:  
96//Hs.20132:AA203113

F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.  
153638:AF010403

F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.0  
0023:357:59//Hs.99948:M97016

F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.  
0e-124:583:99//Hs.27349:AB007917

F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.4  
8:399:58//Hs.22616:AB014564

F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219

F-NT2RP3004472

F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8  
e-152:715:98//Hs.5003:AB007925

F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Sa  
ccharomyces cerevisiae]//4.6e-118:547:99//Hs.124768:AA307735

F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:75  
2:97//Hs.158311:AB012851

F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [M.musculus] //3.5e-  
89:425:99//Hs.126082:AI077718

F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256

F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0  
:370:59//Hs.158244:AB007948

F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.76  
47:M94046

F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110

F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571

F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7  
e-146:679:98//Hs.75970:AB014532

F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1  
e-171:793:98//Hs.74750:AB011126

F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus  
musculus] //2.2e-66:362:94//Hs.125870:AI364967

F-NT2RP3004569

F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRN  
A, complete cds//3.3e-181:860:97//Hs.122752:AF026445

F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0  
e-85:422:97//Hs.129928:AB007923

F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs  
.72160:AJ006266

F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger prote  
in, efp [H.sapiens] //6.4e-13:356:64//Hs.124138:AI266336

F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232

F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56/  
/Hs.79706:U53204

F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436  
 F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98//Hs.118991:AA675919  
 F-NT2RP4000023//ESTs//1.4e-33:182:96//Hs.122722:AA455668  
 F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495  
 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761  
 F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP) //4.9e-13:441:62//Hs.155481:AJ006470  
 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP) //8.0e-151:720:97//Hs.159597:AJ012449  
 F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743  
 F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538  
 F-NT2RP4000111  
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:AB007952  
 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069  
 F-NT2RP4000150  
 F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356  
 F-NT2RP4000159  
 F-NT2RP4000167  
 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946  
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:AB014600  
 F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006  
 F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731

F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.46468:U45984

F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP )//8.6e-158:771:97//Hs.155481:AJ006470

F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:384:89//Hs.115498:AA436298

F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:AF091092

F-NT2RP4000263

F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580

F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481

F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.143648:AB000732

F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112

F-NT2RP4000355

F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:AB018281

F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195

F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073

F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.098:291:59//Hs.994:M95678

F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965

F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368

F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688

F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds  
//0.014:178:66//Hs.125315:AF027156

F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete  
cds//2.0e-34:431:73//Hs.46468:U45984

F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:7  
5//Hs.154326:D42087

F-NT2RP4000449//EST//0.84:113:65//Hs.145274:AI249468

F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:  
J03853

F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-spec  
ific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499

F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151  
:AB001535

F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//  
Hs.78862:D87742

F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete  
cds//0.94:133:69//Hs.159234:U89995

F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2  
//0.60:335:61//Hs.74605:X13293

F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594

F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904

F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partia  
l//2.0e-34:203:93//Hs.99423:AJ010840

F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66/  
/Hs.100837:AB002372

F-NT2RP4000524

F-NT2RP4000528

F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154

F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus] //1.1e-27:162:93//Hs.25597:H93026

F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351

F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053

F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.4214:AF067730

F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513

F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396

F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:60//Hs.144626:AF100907

F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004848

F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783

F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens] //2.8e-46:411:78//Hs.111817:T80622

F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178

F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440

F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058

F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162

F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123

F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939

F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:



438:99//Hs.8173:AC005189

F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833

F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603

F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.75875:U49278

F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367

F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:AI206803

F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843

F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142

F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901

F-NT2RP4000918

F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503

F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//Hs.24812:AF069532

F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371

F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542

F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888

F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058

F-NT2RP4000979

F-NT2RP4000984

F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds

//0.85:257:63//Hs.12956:U90913

F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068

F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204

F-NT2RP4001004

F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718

F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.113287:AF009204

F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494

F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:L40157

F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157

F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP) //7.2e-13:441:63//Hs.155481:AJ006470

F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497

F-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase, partial//1.4e-131:634:98//Hs.106778:AJ010953

F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternative products} //0.025:166:66//Hs.146459:X66975

F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164

F-NT2RP4001095

F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054

F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//2.2e-26:171:92//Hs.14038:R06800

F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//H

s.109804:D64142

F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens] //5.8e-37:185:100//Hs.126925:AA931237

F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.143382:AA476266

F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261

F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207

F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171

F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734

F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324

F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264

F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324

F-NT2RP4001207

F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636

F-NT2RP4001213//KRAB zinc finger protein {alternative products} //1.1e-45 :187:74//Hs.22556:U37251

F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262

F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.122967:AF059569

F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs .106387:AF029778

F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62/- /Hs.75899:D87463

F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59k D, acidic component)//0.015:246:62//Hs.31121:U40571

F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64// Hs.71168:AF070578

F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs .110826:U80736

F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40

) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250

F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917

F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110

F-NT2RP4001339

F-NT2RP4001343

F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39:686:64//Hs.112125:M12625

F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//2.0e-31:784:62//Hs.15432:U53445

F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356

F-NT2RP4001372

F-NT2RP4001373//Homo sapiens clone DtlP1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194

F-NT2RP4001375

F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190

F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918

F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109

F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957

F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:X78933

F-NT2RP4001442

F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:AB018326

F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.26676:AA033997

F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//  
Hs.75533:D10523

F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN  
[H.sapiens]//0.25:216:60//Hs.63220:AA522707

F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395

F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:  
281:61//Hs.5923:X82260

F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:17  
3:94//Hs.5570:AI377863

F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-  
35:329:76//Hs.154970:U03494

F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds  
//0.0015:221:65//Hs.44481:U13220

F-NT2RP4001551//Human BRCA2 region; mRNA sequence CG003//0.56:428:59//Hs  
.30649:U50534

F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174

F-NT2RP4001567

F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN  
MET30-CBR5 INTERGENIC REGION [Saccharomyces cerevisiae]//1.1e-54:252:83/  
/Hs.158208:AA167836

F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410

F-NT2RP4001574

F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98  
//Hs.108826:AL031228

F-NT2RP4001592

F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903

F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952

F-NT2RP4001634

F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN

FKH1-STH1 INTERGENIC REGION [*S.cerevisiae*]//8.6e-57:287:97//Hs.117439:C  
18436

F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.55  
91:AB000409

F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MI  
TOCHONDRIAL PRECURSOR [*Saccharomyces cerevisiae*]//1.0:311:59//Hs.57969:A  
A203629

F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-ma  
f) mRNA, complete cds//0.19:162:67//Hs.30250:AF055376

F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:33  
2:86//Hs.113283:AF018080

F-NT2RP4001696

F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927

F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, comp  
lete cds//0.0035:247:62//Hs.92614:M62302

F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//  
Hs.1285:U08198

F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M  
27878

F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656

F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-3  
4:400:68//Hs.154212:AC004522

F-NT2RP4001803//Human high conductance inward rectifier potassium channe  
l alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069

F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131

F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//  
3.1e-07:509:59//Hs.1572:U11690

F-NT2RP4001828

F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:7

3//Hs.78398:D31888  
 F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749  
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.  
 6e-57:813:65//Hs.6336:AB014572  
 F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens] //4.8e-12:84:94//Hs.140232:AA705170  
 F-NT2RP4001889  
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:  
 97//Hs.15144:AC005014  
 F-NT2RP4001896  
 F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848  
 F-NT2RP4001927  
 F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapien  
 s] //2.8e-54:375:84//Hs.119294:AI379442  
 F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894  
 F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063  
 F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868  
 F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25.  
 Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (l  
 ymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal prot  
 ein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains EST  
 s and GSSs//1.7e-54:788:65//Hs.23796:AL022718  
 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete  
 cds//0.0019:279:65//Hs.159439:AF092047  
 F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila  
 melanogaster] //0.58:463:55//Hs.3826:U69560  
 F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139  
 F-NT2RP4002052  
 F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873

F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA  
 , complete cds//0.97:227:60//Hs.100030:AF002999

F-NT2RP4002075

F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapie  
 ns] //1.0e-38:243:90//Hs.139115:AA325104

F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654

F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152  
 :70//Hs.25180:M96684

F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0  
 e-10:401:59//Hs.89616:M55284

F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204

F-NT2RP4002888

F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960

F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96  
 //Hs.74456:U34995

F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071

F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 s  
 ubunit//0.18:271:60//Hs.139745:U39067

F-NT2RP5003492

F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase  
 , complete cds//6.1e-56:750:69//Hs.132884:AB006179

F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5  
 .1e-14:348:62//Hs.154050:AC004131

F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.9  
 4:202:63//Hs.8152:AB014542

F-NT2RP5003522

F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943

F-NT2RP5003534

F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0



e-69:373:94//Hs.108258:AB007934  
 F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729  
 F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina moschata] /  
 /4.4e-75:355:99//Hs.36727:AI051983  
 F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304  
 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:81  
 5:98//Hs.81449:AF058922  
 F-OVARC1000017//Homo sapiens mRNA for NTAK, complete cds//0.50:482:58//H  
 s.113264:AB005060  
 F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:23  
 8:89//Hs.69469:AF064603  
 F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549  
 F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapi  
 ens] //6.7e-60:305:97//Hs.31696:H50008  
 F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798  
 F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543  
 F-OVARC1000085  
 F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442  
 F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete cds//0.00017:414:59  
 //Hs.106387:AF029778  
 F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600  
 F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans] //2.9e-73:406  
 :92//Hs.109463:AI205174  
 F-OVARC1000109  
 F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48  
 -18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250  
 F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.  
 4e-43:532:72//Hs.118401:AB011134  
 F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010

F-OVARC1000139  
 F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293  
 F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414  
 F-OVARC1000151  
 F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305  
 F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)//0.10:504:59//Hs.154083:U70136  
 F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131  
 F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840  
 F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834  
 F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOLASMIC [Homo sapiens]//2.7e-31:264:79//Hs.151895:AA196379  
 F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984  
 F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.00084:170:65//Hs.107747:AI357868  
 F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306  
 F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287  
 F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECURSOR [Felis catus]//0.51:193:66//Hs.6194:AI378579  
 F-OVARC1000321  
 F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60//Hs.122359:AF051946  
 F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444  
 F-OVARC1000347  
 F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450

F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64/  
/Hs.156016:D50930  
F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162  
F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682  
F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58/  
/Hs.156016:D50930  
F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7e-25:19  
0:84//Hs.139513:AA259082  
F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615  
F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93:281:60//Hs.7  
6279:X53416  
F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//  
Hs.83987:U09284  
F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423  
F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.  
2e-140:566:99//Hs.12334:AB014583  
F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:AI024524  
F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.1  
08112:AF070640  
F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854  
F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926  
F-OVARC1000479  
F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036  
F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327  
F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:53  
9:99//Hs.111285:AF051850  
F-OVARC1000526//ESTs//2.9e-08:368:61//Hs.42771:N26740  
F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492  
F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475

F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667  
 F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410  
 F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA,  
 complete cds//0.87:135:66//Hs.85302:U76421  
 F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358  
 F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200  
 F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729  
 F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63/  
 /Hs.3080:U29725  
 F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722  
 F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881  
 F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097  
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-  
 7 SH2 domain protein, complete cds//1.6e-78:424:93//Hs.86859:D43772  
 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.  
 6e-100:536:94//Hs.111862:AB011162  
 F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:AI277106  
 F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279  
 F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639  
 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds  
 //4.8e-153:549:99//Hs.125315:AF027156  
 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs  
 .4764:AB018306  
 F-OVARC1000700  
 F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320  
 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltra  
 nsferase mRNA, complete cds//1.2e-110:451:91//Hs.13476:AF038661  
 F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]  
 //2.9e-53:318:91//Hs.7049:AI141736

F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411  
 F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196  
 F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H  
 .sapiens]//1.2e-38:194:99//Hs.157059:W28130  
 F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793  
 F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835  
 F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584  
 F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032  
 F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390  
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9  
 e-151:432:100//Hs.155995:AB014543  
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//H  
 s.18910:AF045584  
 F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6  
 .1e-31:183:93//Hs.108620:AA418155  
 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete  
 cds//0.54:133:69//Hs.159234:U89995  
 F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143  
 F-OVARC1000885//EST//0.91:152:63//Hs.160765:AI313323  
 F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777  
 F-OVARC1000890  
 F-OVARC1000891  
 F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818  
 F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:AI376601  
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3  
 e-85:419:97//Hs.9028:AF039691  
 F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456  
 F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//  
 4.3e-64:623:72//Hs.114440:M11119

F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078  
F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.  
sapiens] //2.4e-29:157:97//Hs.136243:AA307843  
F-OVARC1000948  
F-OVARC1000959//EST//0.65:293:55//Hs.134725:AI088986  
F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952  
F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288  
F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:AI283069  
F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2  
557:Y00661  
F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete  
cds//6.8e-10:312:65//Hs.155302:U57317  
F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete  
cds//0.0056:209:62//Hs.10458:AF088219  
F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114  
F-OVARC1001004  
F-OVARC1001010  
F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus] //3.8e-47:2  
34:99//Hs.110327:AA205866  
F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PRO  
TEIN 2//0.0076:624:57//Hs.75063:AL023584  
F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus] //3.  
9e-97:578:89//Hs.111974:AI050735  
F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:  
733:97//Hs.9899:AF099149  
F-OVARC1001040//ESTs//2.2e-38:204:96//Hs.128927:AI168074  
F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385  
F-OVARC1001051  
F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete

cds//1.1e-46:381:81//Hs.154968:U02020  
 F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:AI312873  
 F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans] //1.4e-21:18  
 3:84//Hs.46680:AA809451  
 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial  
 cds//6.6e-132:620:98//Hs.3426:AF082657  
 F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013  
 F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937  
 F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X982  
 48  
 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone I  
 MAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berl  
 in))//1.3e-75:289:95//Hs.21753:AJ005897  
 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//  
 Hs.12912:AF015913  
 F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.  
 1e-151:710:98//Hs.26584:AF051782  
 F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102  
 F-OVARC1001118  
 F-OVARC1001129  
 F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008  
 F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725  
 F-OVARC1001162  
 F-OVARC1001167  
 F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:AI078279  
 F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287  
 F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159  
 F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 P  
 RECURSOR [Homo sapiens] //1.8e-11:192:69//Hs.130020:AA887581

F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//  
Hs.91103:AC005551

F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]  
//1.5e-13:199:71//Hs.109966:C06057

F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN  
VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324:90//Hs.114673:  
W72675

F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889

F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X51688

F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745676

F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424825

F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.75243:D42040

F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:AI377837

F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821

F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224

F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8  
e-144:644:96//Hs.155995:AB014543

F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:35  
5:60//Hs.108812:AA044835

F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172

F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, c  
omplete cds//0.20:188:64//Hs.152455:AF044209

F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264

F-OVARC1001330

F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (eryt  
hrocyte membrane protein band 3-like 1)//0.021:232:62//Hs.79410:U62531

F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:36  
3:99//Hs.105837:AA536054

F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA897493



F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:U67251  
F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198:61//Hs.105940:AF004715  
F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:AI264633  
F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:AI025777  
F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533:74//Hs.109299:AB014554  
F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365:73//Hs.129735:AF010144  
F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//4.1e-149:683:99//Hs.151428:AJ224819  
F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.097:235:65//Hs.25674:AF072242  
F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:U28225  
F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651  
F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586:69//Hs.74597:U52426  
F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651  
F-OVARC1001436  
F-OVARC1001442  
F-OVARC1001453  
F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.110950:AI041823  
F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568  
F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343  
F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//2.6e-86:479:92//Hs.6534:AF016507

F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-9  
7:538:92//Hs.75813:L33243

F-OVARC1001525

F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786

F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595

F-OVARC1001555

F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA/  
/6.8e-57:275:98//Hs.155160:AF031166

F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens]//0.0035:271:60//Hs.108465:AI144299

F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:21  
6:99//Hs.120002:AI038398

F-OVARC1001611

F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500

F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3  
e-37:217:94//Hs.14409:AB011144

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e  
-49:393:81//Hs.95582:AB006867

F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229

F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.4  
28:U03858

F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807

F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863

F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80  
//Hs.155652:X06825

F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588

F-OVARC1001762

F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eI  
F3, p35 subunit mRNA, complete cds//1.4e-150:706:98//Hs.155377:U97670

F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.

8e-117:580:96//Hs.15869:AB014575

F-OVARC1001768//ESTs//0.035:179:64//Hs.87279:AI218697

F-OVARC1001791

F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830

F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI005102

F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.

77:362:58//Hs.116753:AB018287

F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.69949:M94172

F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825

F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453

F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567

F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537

F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973

F-OVARC1001861

F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611

F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709

F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127

F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953

F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.6e-57:300:96//Hs.6216:AF061749

F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834

F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261

F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.8904  
0:U48263

F-OVARC1001928

F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//  
Hs.79706:U53204

F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK6  
52.6 IN CHROMOSOME III [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794

F-OVARC1001949//KRAB zinc finger protein {alternative products} //1.8e-17  
:294:67//Hs.22556:U37251

F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228

F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639

F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens]//1.2e-23:213:78//Hs.105292:AA504776

F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417

F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6  
e-160:739:98//Hs.108258:AB007934

F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865

F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063

F-OVARC1002107

F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7  
e-101:498:96//Hs.75258:AF054174

F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913

F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399  
:62//Hs.112725:AF056022

F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795

F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097

F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:3  
29:58//Hs.107747:AI357868

F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.

00010:300:64//Hs.118929:X79568  
 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:17  
 8:64//Hs.108447:AJ000517  
 F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230  
 F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:AI378928  
 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA,  
 partial cds//1.2e-52:550:72//Hs.42400:AF022789  
 F-PLACE1000014  
 F-PLACE1000031  
 F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088  
 F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494  
 F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755  
 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499  
 F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk1  
 0c10.3 [C.elegans] //1.4e-47:266:93//Hs.30026:AI356771  
 F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING E  
 NTRY !!!! [H.sapiens] //6.4e-15:203:70//Hs.157422:R85366  
 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30  
 :324:60//Hs.76460:U49082  
 F-PLACE1000094  
 F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo  
 sapiens] //6.2e-82:476:92//Hs.111081:AI380378  
 F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens] /  
 /7.7e-27:205:85//Hs.9670:AA632135  
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, compl  
 ete cds//2.5e-151:737:97//Hs.151017:AF058291  
 F-PLACE1000185  
 F-PLACE1000213  
 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255

F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226

F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022

F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202

F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294

F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047

F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675

F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197

F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153

F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024

F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516

F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260

F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174

F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053

F-PLACE1000424

F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590

F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//2.7e-52:421:80//Hs.69747:M35531

F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638

F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60/

/Hs.153014:AB002353

F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573

F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.75578:M85289

F-PLACE1000562

F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538

F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//Hs.21838:AF038179

F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542

F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597:AJ012449

F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751

F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542

F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986

F-PLACE1000636

F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.0e-154:747:96//Hs.5819:AF102265

F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.29595:AJ005896

F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353

F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949

F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447

F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288

F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:33

1:57//Hs.37110:U10694  
 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858  
 F-PLACE1000769  
 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921:AB014548  
 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215  
 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079  
 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189  
 F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180  
 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:U80736  
 F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000  
 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428  
 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455  
 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201  
 F-PLACE1000948  
 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs.80261:L43821  
 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk28h2.5 [C.elegans]//9.3e-45:309:88//Hs.13531:R61789  
 F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.8597:L11672  
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:96//Hs.158497:AB018267  
 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913  
 F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:61//Hs.1974:M92432  
 F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6



940:Z48633

F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876

F-PLACE1001024

F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741

F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:U53204

F-PLACE1001062

F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859

F-PLACE1001088

F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485

F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817

F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:71//Hs.150406:AF022158

F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704

F-PLACE1001168

F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135

F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741

F-PLACE1001238

F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494

F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929

F-PLACE1001272//COATOMER BETA' SUBUNIT//0.012:50:96//Hs.75724:X70476

F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283

F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:58//Hs.124161:AF065164

F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs.16533:D87930

F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:37  
0:60//Hs.42672:AF016052

F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385

F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591

F-PLACE1001351

F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8  
e-26:155:95//Hs.61638:AB018342

F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44  
:393:79//Hs.152005:AF009615

F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748

F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA  
, complete cds//2.6e-09:117:84//Hs.21301:AF093419

F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR  
KINASE SUBSTRATE EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646

F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, co  
mplete CDS//0.0038:496:57//Hs.97681:AJ223333

F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mR  
NA//7.0e-45:456:75//Hs.154069:U06452

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//  
6.5e-71:365:96//Hs.110404:AF091087

F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232

F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987

F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510

F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455

F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716

F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529

F-PLACE1001503

F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914

F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753

F-PLACE1001545

F-PLACE1001551

F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835

F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233

F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987

F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230

F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005

F-PLACE1001611//Human faciogenital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690

F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:AB018341

F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198

F-PLACE1001640

F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927

F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250

F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI125696

F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.101555:U93869

F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776

F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686

F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094

F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.

1480:M60052

F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159

F-PLACE1001745

F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361

F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/  
/2.8e-160:773:97//Hs.4812:AF061243

F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-3  
5:269:83//Hs.5247:AF029750

F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283

F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, comp  
lete cds//3.4e-52:548:72//Hs.150981:U47050

F-PLACE1001781

F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115

F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138

F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta s  
ubunit (SCS) mRNA, partial cds//3.6e-110:546:96//Hs.40820:AF058953

F-PLACE1001821

F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494

F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214

F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906

F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257

F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220

F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cd  
s//4.0e-153:685:95//Hs.17839:AF099936

F-PLACE1001928//H.sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837

F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58  
//Hs.106387:AF029778

F-PLACE1001989

F-PLACE1002004

F-PLACE1002046

F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465  
:58//Hs.153322:D42108

F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555

F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2  
e-39:635:64//Hs.38176:AB011178

F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA  
, complete cds//4.3e-83:388:99//Hs.5171:AF069765

F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637

F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.  
2e-13:384:61//Hs.737:M62831

F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSO  
R [Homo sapiens] //0.89:60:75//Hs.144290:T61747

F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631

F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:7  
9//Hs.40100:AB002390

F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891

F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627

F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674

F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.9079  
8:U79289

F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989

F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI024442

F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935

F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3  
e-75:434:83//Hs.23094:M19503

F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675

F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279

F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291  
 F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710  
 F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067  
 F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458:66//Hs.40993:AF000148  
 F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI368947  
 F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:66//Hs.150406:AF022158  
 F-PLACE1002465  
 F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:AJ007581  
 F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523  
 F-PLACE1002493  
 F-PLACE1002499  
 F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.111967:U76010  
 F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482  
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:AB018256  
 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566:96//Hs.99348:AC004774  
 F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369  
 F-PLACE1002571//Homo sapiens mRNA for TP53, complete cds//0.99:274:59//Hs.138202:AF027866  
 F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627  
 F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI393725  
 F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:D44497

F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187  
 F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI198915  
 F-PLACE1002625  
 F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04  
 412  
 F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706  
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternativ  
 ely spliced, complete cds//1.1e-187:804:97//Hs.124903:AF068180  
 F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903  
 F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complet  
 e cds//0.34:230:58//Hs.159196:U92971  
 F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080  
 F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728  
 F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827  
 F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, comple  
 te cds//0.0031:298:62//Hs.26285:AF082516  
 F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:AI368926  
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:7  
 0//Hs.77546:D79994  
 F-PLACE1002815  
 F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3  
 e-70:687:73//Hs.9028:AF039691  
 F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:AI089163  
 F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:AI334167  
 F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405  
 F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024  
 F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627  
 F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:AI040029  
 F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056

F-PLACE1002962

F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus] /  
/0.031:372:59//Hs.8021:AI041815

F-PLACE1002991

F-PLACE1002993

F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans] //1.3e-12:104  
:86//Hs.124808:T86959

F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0510//0.99:192:64//Hs.92660:AB007979

F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0  
e-131:632:97//Hs.129872:AB011088

F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7  
e-14:555:58//Hs.154740:AB014567

F-PLACE1003045

F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491

F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//  
Hs.102137:U31875

F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419

F-PLACE1003136

F-PLACE1003145

F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590

F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997

F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797

F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransfe  
rase mRNA, complete cds//0.98:221:60//Hs.139756:U59209

F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532

F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:AI208770

F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208

F-PLACE1003249//Insulin-like growth factor 1 (somatomedia C)//0.99:175:6



2//Hs.85112:X57025

F-PLACE1003256

F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802

F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106

F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.37138:U35376

F-PLACE1003334

F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308

F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568

F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715

F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:78//Hs.163820:H71277

F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575

F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858

F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009

F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069

F-PLACE1003383

F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:94//Hs.125175:AI142546

F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178

F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like) //0.40:206:62//Hs.30223:X90846

F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912

F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874

F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635

F-PLACE1003516//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//

3.4e-85:357:86//Hs.103948:K00627  
 F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145  
 F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6  
 940:Z48633  
 F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248  
 F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:54  
 3:97//Hs.120416:AA057428  
 F-PLACE1003553  
 F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780  
 F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:4  
 99:58//Hs.65993:AF000367  
 F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932  
 F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194  
 F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARNING ENT  
 RY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620  
 F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965  
 F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.896  
 50:L38961  
 F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97  
 //Hs.56851:D83200  
 F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00  
 065:236:64//Hs.22116:AF064104  
 F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896  
 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3  
 e-122:737:87//Hs.23094:M19503  
 F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105  
 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762  
 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.  
 021:445:58//Hs.158275:AI365413

F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56/  
/Hs.76730:AB002299

F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1  
.4e-133:669:95//Hs.98658:AF053305

F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101

F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor pro  
tein//8.5e-09:393:60//Hs.103527:AJ000553

F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapien  
s]//1.8e-53:260:99//Hs.102928:AI346344

F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648

F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983

F-PLACE1003768//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//  
2.7e-40:608:68//Hs.139107:K00629

F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944

F-PLACE1003783

F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0  
:457:57//Hs.62318:AB018308

F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:3  
14:60//Hs.1050:M85169

F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201  
:68//Hs.40806:AA018786

F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165

F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124

F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359

F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257

F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770

F-PLACE1003886

F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:70  
2:67//Hs.153322:D42108

F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050  
 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944  
 F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142  
 F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCH  
 ONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F  
 03069  
 F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585  
 F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537  
 F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536  
 F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit m  
 RNA, complete cds//2.0e-47:522:71//Hs.3136:U42412  
 F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812  
 F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940  
 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516  
 F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration o  
 ncogene spil//0.85:164:64//Hs.153045:X52056  
 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta pol  
 ypeptide 1//3.1e-41:422:74//Hs.3620:X04526  
 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418  
 :96//Hs.156161:AI333779  
 F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552  
 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64/  
 /Hs.76986:D83785  
 F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666  
 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201  
 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precu  
 sor, mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493  
 F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722  
 F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273

F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689

F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R. norvegicus]//1.1e-98:479:97//Hs.31718:N29128

F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736

F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139:AB007914

F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds//2.0e-157:756:97//Hs.127007:AF084830

F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884

F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576

F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588

F-PLACE1004336

F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153

F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552

F-PLACE1004384//Human HsLIM15 mRNA for HsLim15, complete cds//2.0e-49:466:76//Hs.37181:D64108

F-PLACE1004388

F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871

F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579

F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190

F-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete

cds//9.9e-131:536:99//Hs.155410:U49283  
 F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867  
 F-PLACE1004460  
 F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363  
 F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085  
 F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416  
 F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163  
 F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680  
 F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699:97//Hs.122752:AF026445  
 F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150  
 F-PLACE1004518  
 F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314  
 F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854  
 F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371  
 F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299  
 F-PLACE1004645  
 F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991  
 F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590  
 F-PLACE1004664  
 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563  
 F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035606  
 F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589  
 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561

F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.  
48483:AF007131

F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:9  
6:71//Hs.125740:AA884845

F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542

F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891

F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148

F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680

F-PLACE1004743

F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,  
4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:2  
60:90//Hs.6863:W52470

F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-1  
72:828:97//Hs.104715:AF084367

F-PLACE1004777//Human myosin-IXb mRNA, complete cds//1.0e-29:556:63//Hs.  
159629:U42391

F-PLACE1004793

F-PLACE1004804

F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340

F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTE  
IN 70 KD [Xenopus laevis]//2.4e-78:415:95//Hs.80965:AA493284

F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:  
69//Hs.22111:AB002362

F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047

F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943

F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:33  
8:57//Hs.8546:U97669

F-PLACE1004838

F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//

0.89:200:66//Hs.21537:X80910  
 F-PLACE1004868  
 F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772  
 F-PLACE1004900  
 F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382  
 F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929  
 F-PLACE1004918//Human tumor susceptiblity protein (TSG101) mRNA, complet  
 e cds//4.1e-24:402:64//Hs.118910:U82130  
 F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cd  
 s//9.7e-86:519:88//Hs.17839:AF099936  
 F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592  
 F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851  
 F-PLACE1004969  
 F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protei  
 n RI58 mRNA, complete cds//0.031:235:60//Hs.27610:U34605  
 F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.  
 9e-43:331:83//Hs.153468:AB011147  
 F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520  
 F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831  
 F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459  
 F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159  
 F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943  
 F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594  
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2  
 e-161:761:98//Hs.14687:AB011148  
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete  
 cds//3.0e-11:757:56//Hs.122967:AF059569  
 F-PLACE1005077//EST//0.79:283:59//Hs.89276:AA283899  
 F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740



F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.  
9e-49:401:80//Hs.153468:AB011147

F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20  
:194:80//Hs.75437:L40401

F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding  
protein (FBI1) mRNA, complete cds//8.9e-18:538:62//Hs.104640:AF000561

F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:4  
05:57//Hs.73166:U76366

F-PLACE1005111//ESTs//0.66:191:63//Hs.106446:N93227

F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//H  
s.2557:Y00661

F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapie  
ns]//4.8e-12:360:63//Hs.142177:H11741

F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:7  
2//Hs.154326:D42087

F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.  
82:259:60//Hs.128316:AB014541

F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.eleg  
ans]//4.4e-126:583:99//Hs.25347:AI138605

F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417

F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009

F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47  
-1 [D.melanogaster]//0.56:192:60//Hs.47334:W72370

F-PLACE1005243

F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941

F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M  
97252

F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1  
e-150:706:98//Hs.118087:AB011182

F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947  
 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66  
 //Hs.101642:X60673  
 F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//  
 0.83:239:62//Hs.80684:X62534  
 F-PLACE1005313  
 F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.eleg  
 ans]//6.0e-81:459:91//Hs.146177:R51650  
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:8  
 8//Hs.134031:AC004794  
 F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.9  
 6:510:56//Hs.159183:AB018297  
 F-PLACE1005373  
 F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348  
 F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751  
 F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951  
 F-PLACE1005467//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.740  
 95:L20433  
 F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925  
 F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5  
 e-126:744:87//Hs.23094:M19503  
 F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323  
 F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA707973  
 F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029  
 F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105  
 F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747  
 F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572  
 F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335  
 F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385

F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144

F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae] //4.5e-51:258:97//Hs.7736:W81261

F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278

F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436

F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594

F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851

F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans] //3.5e-32:197:92//Hs.8241:AA283057

F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234

F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867

F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991

F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:AF083255

F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618

F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:AB007917

F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457

F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437

F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944

F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//Hs.75111:D87258

F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302

F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIO

ESTERASE, MEDIUM CHAIN [Rattus norvegicus] //5.7e-49:252:88//Hs.24309:AI1  
25696

F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493

F-PLACE1005802

F-PLACE1005803

F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds  
//4.5e-128:636:96//Hs.125315:AF027156

F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//  
8.4e-156:739:98//Hs.11183:AF065482

F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens] //4.1e-42:327:81//Hs.138404:R70986

F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58/  
/Hs.75770:L41870

F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497

F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905

F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242

F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487

F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552

F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300

F-PLACE1005898

F-PLACE1005921

F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504

F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274

F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342  
:57//Hs.89839:M18391

F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142

F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:  
X69978

F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357

F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468  
F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:  
66//Hs.107747:AI357868  
F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, co  
mplete cds//1.0:215:63//Hs.7885:U13948  
F-PLACE1005968  
F-PLACE1005990  
F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:  
312:77//Hs.42674:U61981  
F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256  
F-PLACE1006011  
F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743  
F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.  
021:202:64//Hs.158319:AB018332  
F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97  
//Hs.98782:X99906  
F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395  
F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//  
4.1e-147:679:99//Hs.4976:AF039023  
F-PLACE1006129  
F-PLACE1006139  
F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:  
79//Hs.153014:AB002353  
F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.  
sapiens]//2.9e-12:119:84//Hs.23153:R92857  
F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868  
F-PLACE1006164//ESTs//0.099:223:60//Hs.8108:AA902721  
F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:9  
2//Hs.152894:AC005239

F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:AI074005  
 F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:  
 99//Hs.30464:AF091433  
 F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608  
 F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation fac  
 tor 4A-II homolog//3.5e-59:369:88//Hs.135623:AA134719  
 F-PLACE1006205  
 F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH F  
 ACTOR 1 [H.sapiens]//0.0089:166:63//Hs.127179:AI279486  
 F-PLACE1006225  
 F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668  
 F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185  
 F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802  
 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3  
 e-168:791:98//Hs.31921:AB014548  
 F-PLACE1006262  
 F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.  
 7277:AJ001625  
 F-PLACE1006318  
 F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503  
 F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:AI361492  
 F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249  
 F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481  
 F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.  
 153529:AF070581  
 F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete c  
 ds//2.6e-07:403:61//Hs.105940:AF004715  
 F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693  
 F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:9

7//Hs.22396:AF062085

F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:

74//Hs.21560:AB002296

F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.131846:AF069735

F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:AB011129

F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866

F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381

F-PLACE1006470

F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194

F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511

F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493

F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584

F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542

F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358

F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:AI356219

F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784

F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529

F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:AB018280

F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781:99//Hs.155377:U97670

F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088  
 F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858  
 F-PLACE1006629//Homo sapiens (clone s22i71) mRNA fragment//0.097:229:63/  
 /Hs.26956:L40396  
 F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:AI131473  
 F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]  
 //1.6e-12:113:83//Hs.3385:N25917  
 F-PLACE1006678  
 F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153  
 638:AF010403  
 F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1  
 .6e-05:382:63//Hs.43627:U35612  
 F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354  
 F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152  
 F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M  
 97252  
 F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:AI075783  
 F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:AI051228  
 F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10  
 :84:95//Hs.123642:M83941  
 F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:AI422017  
 F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892  
 F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.  
 47:403:56//Hs.15832:AB014518  
 F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7  
 e-103:619:87//Hs.23094:M19503  
 F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876  
 F-PLACE1006860//EST//0.0062:206:65//Hs.158793:AI376773  
 F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273



F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.  
0:268:58//Hs.5333:AB018254

F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601

F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI089187

F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443

F-PLACE1006917

F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913

F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211

F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565

F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127:L12723

F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae] //3.2e-07:67:98//Hs.21806:AA630312

F-PLACE1006962//H.sapiens irlB mRNA//2.3e-16:202:71//Hs.135202:X63417

F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c)  
) mRNA, complete cds//0.14:191:67//Hs.8813:AF032922

F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753

F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei  
(ENT2) mRNA, complete cds//3.1e-05:594:58//Hs.32951:AF034102

F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971

F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0  
e-117:775:84//Hs.23094:M19503

F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.1298  
11:AJ223957

F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:3  
61:60//Hs.75813:L33243

F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987

F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glyco  
gen debranching enzyme, glycogen storage disease type III)//0.18:268:63/  
/Hs.904:U84010

F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385  
 F-PLACE1007112  
 F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:AI160121  
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78  
 869:M81601  
 F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965  
 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090  
 :412:59//Hs.8546:U97669  
 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64  
 //Hs.79706:U53204  
 F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-  
 II-T1, complete cds//2.0e-58:405:87//Hs.80598:D50495  
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141  
 F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467  
 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//  
 Hs.121556:Y15909  
 F-PLACE1007274  
 F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syn  
 drome)//0.94:167:64//Hs.606:L06133  
 F-PLACE1007282  
 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436  
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412  
 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA,  
 complete cds//0.88:298:58//Hs.144877:AF029403  
 F-PLACE1007342  
 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mR  
 NA, complete cds//1.7e-121:567:98//Hs.76596:AF096870  
 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77/  
 /Hs.19949:X98173

F-PLACE1007375  
 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642  
 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287  
 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//Hs.14387:AF093771  
 F-PLACE1007416  
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436  
 F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359  
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93/  
 /Hs.6445:L40391  
 F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714  
 F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103  
 F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975  
 F-PLACE1007488  
 F-PLACE1007507//ESTs//1.2e-99:274:98//Hs.123462:AA903385  
 F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503  
 F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296  
 F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979  
 F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468:5  
 7//Hs.113283:AF018080  
 F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:AI076755  
 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.  
 0e-70:733:71//Hs.65238:AB014561  
 F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863  
 F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257  
 F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI089163  
 F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2  
 e-12:778:56//Hs.33010:AB014533  
 F-PLACE1007621

F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867  
 F-PLACE1007645  
 F-PLACE1007649  
 F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266  
 F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI027055  
 F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:AI348503  
 F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63  
 //Hs.1103:X02812  
 F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.757  
 89:D87953  
 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/  
 /4.1e-149:709:97//Hs.4812:AF061243  
 F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.eleg  
 ans] //4.5e-36:233:89//Hs.108797:AA476815  
 F-PLACE1007729//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE  
 [H.sapiens] //0.00033:270:64//Hs.104129:AA923278  
 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.  
 6e-156:728:98//Hs.153121:AB014585  
 F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:6  
 8//Hs.159347:M62424  
 F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030  
 F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:AI089469  
 F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656  
 F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504  
 F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107  
 F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841  
 F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261635  
 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3  
 e-38:396:77//Hs.23094:M19503

F-PLACE1007852

F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.

3e-190:894:98//Hs.28020:AB018309

F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:AI038387

F-PLACE1007877

F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943

F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA

0487//7.3e-156:755:97//Hs.92381:AB007956

F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002

F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538

F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.5671:AF084530

F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:730:98//Hs.78106:AF079529

F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens] //5.1e-45:264:92//Hs.42222:W28567

F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:AI097043

F-PLACE1008000//Homo sapiens veli 1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:AF087693

F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031

F-PLACE1008044

F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382

F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:U44060

F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds //1.0:461:58//Hs.155494:U60975

F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.100431:AF044197

F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769

F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874  
 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI218683  
 F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.1e-20:124:95//Hs.146238:AI263135  
 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427  
 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524  
 F-PLACE1008201  
 F-PLACE1008209  
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856  
 F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385  
 F-PLACE1008273  
 F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113  
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970  
 F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287  
 F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071  
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129  
 F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362  
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579  
 F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569  
 F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911  
 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171  
 F-PLACE1008398

F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA  
, complete cds//2.5e-09:461:62//Hs.25674:AF072242

F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:9  
8//Hs.7763:D86326

F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943

F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-2  
6.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro  
/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contai  
ns ESTs, STSS, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.5792  
2:AL023653

F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499

F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, ep  
idermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]//0.019:530:58  
//Hs.72248:S72487

F-PLACE1008437

F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335

F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901

F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63  
//Hs.27590:AB002381

F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds/  
/6.8e-07:469:60//Hs.1177:U10886

F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TAS  
K) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823

F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI274697

F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081

F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-  
45:507:71//Hs.8003:AC004997

F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.  
0:95:71//Hs.117546:U31767

F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:AI283069

F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175:812:98//Hs.23255:AB018334

F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens] //1.2e-15:350:66//Hs.151087:AA649326

F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794

F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560

F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458

F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211

F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394

F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535

F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.147967:AF044333

F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728

F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.90443:AF038406

F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741

F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080

F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus] //4.3e-17:285:69//Hs.35460:H65503

F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds //1.4e-121:503:97//Hs.6458:AF060543

F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens] //0.30:127:68//Hs.111380:AA258772

F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542

F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:376:98//Hs.7179:AF011905



F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883

F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1 / thailand)]//0.73:354:59//Hs.26322:AA156858

F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:AI052728

F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:AI221563

F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503

F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323

F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318:AB018308

F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W84771

F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026

F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937

F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:U75308

F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950

F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112

F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762

F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689

F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689:S70585

F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:AI239698

F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:AI090525

F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800

F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091

F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:AI337031

F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011  
 F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:AI040890  
 F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788  
 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3  
 (XRCC3) mRNA, complete cds//1.1e-139:671:97//Hs.99742:AF035586  
 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:  
 59//Hs.35804:D25215  
 F-PLACE1009150//Human HsLIM15 mRNA for HsLim15, complete cds//1.7e-50:44  
 0:78//Hs.37181:D64108  
 F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
 0484//4.0e-46:440:69//Hs.158095:AB007953  
 F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, comp  
 lete cds//0.28:245:61//Hs.92614:M62302  
 F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250  
 F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770  
 F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:AI282821  
 F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100  
 F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.eleg  
 ans] //3.6e-117:588:95//Hs.54943:Z78396  
 F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689  
 F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131  
 F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.1  
 46403:M29540  
 F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575  
 F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Sa  
 ccharomyces cerevisiae] //1.9e-21:121:98//Hs.124768:AA307735  
 F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338  
 F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mR  
 NA, complete cds//9.7e-08:411:59//Hs.23731:U83192

F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3  
e-91:594:86//Hs.23094:M19503

F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767

F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473

F-PLACE1009368

F-PLACE1009375

F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81/  
/Hs.43681:AL022394

F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M  
27878

F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101  
174:AF047863

F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:2  
10:86//Hs.3404:AF035262

F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:  
68//Hs.155291:D13630

F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:5  
8//Hs.82128:AJ012159

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.  
76987:AF012872

F-PLACE1009459//H.sapiens gap gene mRNA, complete CDS//1.0:241:60//Hs.1  
51641:Z24680

F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS  
E BETA 2//0.00039:347:60//Hs.994:M95678

F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//4.  
1e-91:464:96//Hs.155049:AC004531

F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:AI308839

F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:  
63//Hs.16165:AB002405

F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:U70728

F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417

F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:AI416956

F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866

F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291

F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806

F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:66//Hs.13889:AI341394

F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080

F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:AI074011

F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:AI094085

F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773

F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087

F-PLACE1009639

F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:AB011159

F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494

F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534

F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926

F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650

F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789

F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024

F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989

F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25  
-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3,  
EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein  
Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part o  
f a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C  
. elegans C16A3.8. Contains ESTs and GSSs//5.5e-130:600:95//Hs.16411:AL0  
30996

F-PLACE1009845

F-PLACE1009861

F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021

F-PLACE1009886

F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889

F-PLACE1009908

F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X6371  
7

F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379

F-PLACE1009925

F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153

F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446

F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0  
.89:243:61//Hs.127610:Z80345

F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114

F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174  
:88//Hs.11449:AI201540

F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7  
e-36:196:96//Hs.153545:AB014529

F-PLACE1010023

F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878

F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H. sapiens] //5.2e-63:312:98//Hs.142151:AA984061

F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:AF065482

F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925

F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus musculus] //1.8e-38:212:95//Hs.98067:AA236822

F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R. norvegicus] //1.8e-08:100:89//Hs.11469:U69567

F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:AF020761

F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.122967:AF059569

F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682

F-PLACE1010134//H. sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889

F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740

F-PLACE1010152

F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792

F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582

F-PLACE1010202//ESTs, Weakly similar to No definition line found [C. elegans] //2.3e-72:391:94//Hs.35225:H69637

F-PLACE1010231

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:AB007917

F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590

F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149  
:93//Hs.11449:AI201540

F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813

F-PLACE1010310//HOMEBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74  
095:L20433

F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:  
U76248

F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659

F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117

F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855

F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648

F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986

F-PLACE1010401

F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61/  
/Hs.125257:U70824

F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete c  
ds//7.2e-152:702:99//Hs.13313:AF039081

F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500

F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100

F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein m  
RNA, complete cds//1.0:175:64//Hs.159273:AF054177

F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472

F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979

F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148

F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA  
HELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229  
:N44661

F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14

p (PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186  
 F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394  
 F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858  
 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61  
 //Hs.106387:AF029778  
 F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//  
 0.012:258:62//Hs.144375:AA484200  
 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461  
 F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225  
 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5  
 e-66:363:95//Hs.10801:AB011102  
 F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076  
 F-PLACE1010662  
 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, com  
 plete cds//1.1e-74:697:74//Hs.37138:U35376  
 F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027  
 F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mR  
 NA, partial cds//6.1e-77:393:96//Hs.50758:AF092564  
 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), pa  
 rtial//0.97:314:59//Hs.14574:AJ131244  
 F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.  
 159629:U42391  
 F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTE  
 IN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284  
 F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTE  
 IN HCNGP [Mus musculus]//6.0e-45:251:94//Hs.11379:AA594140  
 F-PLACE1010786  
 F-PLACE1010800  
 F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157



F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085  
F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1  
[H.sapiens] //2.9e-28:245:79//Hs.132736:AA583494  
F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048  
F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel.  
[H.sapiens] //5.8e-67:336:97//Hs.130135:AA905493  
F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:  
X59244  
F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7  
e-149:694:98//Hs.118087:AB011182  
F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671  
F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:1  
67:65//Hs.1050:M85169  
F-PLACE1010900  
F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981  
F-PLACE1010917  
F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537  
F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1  
e-139:653:98//Hs.74750:AB011126  
F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//  
2.9e-91:437:98//Hs.66392:AF064244  
F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985  
F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154  
F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444:59/  
/Hs.585:X04506  
F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632  
F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721  
F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931  
F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032

F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds/  
/0.28:179:67//Hs.1177:U10886

F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS  
E BETA 2//6.2e-11:207:68//Hs.994:M95678

F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-  
35:310:78//Hs.2407:Z49194

F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk)  
mRNA, complete cds//0.74:228:61//Hs.153640:U56998

F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320

F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663

F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037

F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317

F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370857

F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949

F-PLACE1011160

F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443

F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114

F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransfe  
rase mRNA, complete cds//6.9e-124:576:99//Hs.159140:AF038664

F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7e-101:4  
69:99//Hs.8241:AA283057

F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEE  
SL70F [C.elegans]//2.6e-62:221:88//Hs.101821:W27452

F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751

F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4  
e-147:675:99//Hs.23168:AB011101

F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:9  
8//Hs.15144:AC005014

F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803

F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191:65//Hs.140950:AF070637

F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915

F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160

F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310

F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:99//Hs.5819:AF102265

F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs.159897:AB007970

F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535

F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Ra w3 [R.norvegicus]//6.7e-68:325:99//Hs.107245:AA627053

F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868

F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552

F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801:AB011102

F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557:72//Hs.23094:M19503

F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:AI025204

F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703:99//Hs.111138:AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482

F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264

F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997

F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319

F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476

F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333

F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180

F-PLACE1011586//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462

F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778

F-PLACE1011641

F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631

F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661

F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086

F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745

F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234

F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366

F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350

F-PLACE1011725

F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853

F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891

F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240

F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693

F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660

F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664

F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775

F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152

F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913  
 F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:4  
 78:56//Hs.107747:AI357868  
 F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817  
 F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//  
 3.7e-140:664:98//Hs.3838:AF059617  
 F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763  
 F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514  
 F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591  
 F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514  
 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0  
 e-148:690:98//Hs.88756:AB018256  
 F-PLACE20000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
 0487//6.5e-54:290:81//Hs.92381:AB007956  
 F-PLACE20000006//ESTs//0.067:224:62//Hs.144100:AI205503  
 F-PLACE20000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330  
 F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627  
 F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831  
 F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627  
 F-PLACE2000017  
 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose  
 polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557  
 F-PLACE2000030  
 F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.8  
 5:234:66//Hs.11342:U91512  
 F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.0  
 58:348:62//Hs.94653:AB011179  
 F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59/  
 /Hs.79706:U53204

F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128  
F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966  
F-PLACE2000061  
F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:6  
62:86//Hs.23759:M98457  
F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7  
.1e-135:631:98//Hs.9443:AF027219  
F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333  
F-PLACE2000100  
F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219  
F-PLACE2000111//H.sapiens mRNA for 1-acylglycerol-3-phosphate O-acyltran  
sferase//0.76:215:65//Hs.6587:U56417  
F-PLACE2000115  
F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:  
79//Hs.153014:AB002353  
F-PLACE2000132  
F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H.sapi  
ens]//1.2e-08:245:64//Hs.140343:AA718911  
F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U546  
45  
F-PLACE2000164  
F-PLACE2000170  
F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179  
F-PLACE2000176  
F-PLACE2000187  
F-PLACE2000216  
F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933  
F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:  
63//Hs.21560:AB002296

F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338

F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:AB007958

F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522

F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560

F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869

F-PLACE2000317

F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:M89796

F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088

F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299

F-PLACE2000347//ESTs, Moderately similar to F18547\_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817

F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645

F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045

F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861

F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032

F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638

F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.158095:AB007953

F-PLACE2000398

F-PLACE2000399

F-PLACE2000404

F-PLACE2000411

F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:46

3:74//Hs.113283:AF018080  
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966  
 F-PLACE2000427  
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719  
 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257  
 F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalact  
 osaminyltransferase (T2)//1.9e-20:418:64//Hs.130181:X85019  
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:32  
 4:81//Hs.113283:AF018080  
 F-PLACE2000455//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN  
 G ENTRY !!!! [H.sapiens]//4.0e-05:100:73//Hs.104239:AA488082  
 F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107  
 :X87241  
 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381  
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:52  
 0:81//Hs.113283:AF018080  
 F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:20  
 4:73//Hs.46925:Y10262  
 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:  
 69//Hs.101359:AB002384  
 F-PLACE3000020//Prostaglandin I2 (prostacyclin) receptor (IP)//0.00081:5  
 00:61//Hs.393:D38128  
 F-PLACE3000029  
 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248  
 F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842  
 F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRN  
 A, complete cds//1.0:186:62//Hs.122752:AF026445  
 F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8  
 e-48:283:83//Hs.23711:AB018295



F-PLACE3000121

F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081

F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603

F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243

F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016

F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871

F-PLACE3000148

F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:AB014572

F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023

F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:U79666

F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:AB011147

F-PLACE3000160

F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219

F-PLACE3000194

F-PLACE3000197

F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546

F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975

F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//Hs.77522:X62744

F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216

F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377

F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF40) mRNA, complete cds//9.2e-56:200:85//Hs.133089:AF064019

F-PLACE3000226

F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046

F-PLACE3000244

F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858

F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650

F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944

F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770

F-PLACE3000310

F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586

F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219

F-PLACE3000331

F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:AB014545

F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741

F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355

F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194

F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:234:63//Hs.7498:U41514

F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441

F-PLACE3000363

F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928

F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641  
 F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432  
 F-PLACE3000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73  
 919:X81637  
 F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785  
 F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270  
 F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715  
 F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541  
 F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apa  
 f-1) mRNA, complete cds//1.9e-07:116:78//Hs.77579:AF013263  
 F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens  
 ]//1.6e-51:260:98//Hs.122512:H61502  
 F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.  
 00020:630:57//Hs.17585:AB018344  
 F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161  
 F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of comp  
 lex II, complete cds//3.6e-32:183:93//Hs.108326:AB006202  
 F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874  
 F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs  
 .117572:U94888  
 F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190  
 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6  
 e-118:331:100//Hs.105399:AB018352  
 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1  
 .1e-06:244:63//Hs.154050:AC004131  
 F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//  
 Hs.139088:AF070533  
 F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, comp  
 lete cds//1.4e-53:669:67//Hs.40993:AF000148

F-PLACE4000063  
 F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713  
 F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819  
 F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058  
 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8  
 e-147:684:99//Hs.129937:AB007931  
 F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.  
 98614:AF006751  
 F-PLACE4000129  
 F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627  
 F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856  
 F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//  
 Hs.69740:U09367  
 F-PLACE4000192  
 F-PLACE4000211  
 F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594  
 F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:6  
 0//Hs.146395:AB002329  
 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317  
 F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40  
 ) mRNA, nuclear gene encoding mitochondrial protein, complete cds//0.009  
 5:156:69//Hs.30928:AF043250  
 F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609  
 F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886  
 F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2  
 e-27:191:87//Hs.2397:Z70200  
 F-PLACE4000261  
 F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk5  
 2b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645

F-PLACE4000270

F-PLACE4000300

F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966

F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365

F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292

F-PLACE4000367

F-PLACE4000369

F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256

F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823

F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046

F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026:AB014540

F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:AI275982

F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263:92//Hs.2397:Z70200

F-PLACE4000445

F-PLACE4000450

F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874

F-PLACE4000487//Sialophorin (gpL115, leukosialin, CD43)//3.0e-14:189:71//Hs.80738:X52075

F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951

F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289

F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731

F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022

F-PLACE4000548

F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript  
//0.0035:510:59//Hs.39163:AF000986

F-PLACE4000581

F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine  
leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:AI034080

F-PLACE4000593//ESTs, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239  
:79//Hs.109084:AI004675

F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074

F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.  
5e-47:562:69//Hs.129685:AB002446

F-PLACE4000650

F-PLACE4000654

F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132

F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05  
299

F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HO  
MOLOG 50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.118634:U66688

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5  
e-148:706:98//Hs.109299:AB014554

F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:  
M23254

F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877

F-THYR01000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//H  
s.3989:AB002313

F-THYR01000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-  
35:299:81//Hs.2407:Z49194

F-THYR01000034

F-THYR01000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099

F-THYR01000040//ESTs//0.30:331:59//Hs.87176:AI148326

F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63  
//Hs.101996:AB002345  
F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//  
Hs.6654:AB014557  
F-THYRO1000085  
F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065  
F-THYRO1000107  
F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8  
e-106:690:86//Hs.23094:M19503  
F-THYRO1000121  
F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//  
Hs.103502:U70732  
F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//2.8e-  
155:732:98//Hs.87619:AF087142  
F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203  
F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416  
F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs  
.155464:AF088219  
F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete  
cds//1.1e-05:261:61//Hs.152936:D63475  
F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:27  
0:87//Hs.101238:Y11312  
F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270  
F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883  
F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4  
e-175:805:99//Hs.43445:AJ005698  
F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.  
0e-88:616:84//Hs.79672:AB014552  
F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848

F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:  
U79297

F-THYRO1000241//EST//0.48:102:69//Hs.160764:AI313322

F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M  
27878

F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.6  
1:211:64//Hs.60103:AB014590

F-THYRO1000270

F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:  
848:98//Hs.25846:AB016068

F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxyla  
se [C.elegans]//7.6e-92:431:99//Hs.122719:AA777803

F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.8  
0731:M63175

F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2  
e-164:763:98//Hs.12002:AB018333

F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds  
//6.9e-34:177:84//Hs.7833:U29091

F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919

F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.  
081:240:62//Hs.118401:AB011134

F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855

F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.eleg  
ans]//5.8e-39:245:91//Hs.119095:T79413

F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572

F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238

F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773

F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.09



6:306:60//Hs.155024:U00115

F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X5252  
0

F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-2  
2:248:76//Hs.162011:AA513663

F-THYRO1000488

F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200

F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298

F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120

F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877

F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protei  
n 4, complete cds//0.28:229:61//Hs.100058:AB006713

F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949

F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete  
cds//2.4e-168:808:97//Hs.151411:AF075587

F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322

F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331

F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2  
685:Z50053

F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081

F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941

F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125

F-THYRO1000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,  
3429 nt]//1.8e-09:127:77//Hs.116007:S79267

F-THYRO1000662

F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157

F-THYRO1000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,  
3429 nt]//5.7e-49:281:77//Hs.116007:S79267

F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46

:368:57//Hs.26557:AA480380  
F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452  
F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324  
F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59  
//Hs.79706:U53204  
F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085  
F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74  
//Hs.7977:AB007871  
F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1  
.0:209:62//Hs.19492:AF061573  
F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:5  
7//Hs.158132:D63481  
F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC  
41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084  
F-THYRO1000787  
F-THYRO1000793  
F-THYRO1000796  
F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.  
4e-36:561:68//Hs.129685:AB002446  
F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:7  
5//Hs.154326:D42087  
F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339  
F-THYRO1000843  
F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788  
F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170  
F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103  
F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531  
F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA

0487//1.8e-43:318:79//Hs.92381:AB007956  
 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)  
 mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529  
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79  
 217:M77836  
 F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs  
 .112432:AC005263  
 F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65/  
 /Hs.83558:D86963  
 F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA he  
 licase (SUV3) mRNA, nuclear gene encoding mitochondrial protein, complet  
 e cds//2.7e-15:123:90//Hs.106469:AF042169  
 F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907  
 F-THYRO1000983  
 F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646  
 F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307  
 F-THYRO1001003  
 F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124  
 :AF019369  
 F-THYRO1001033//H.sapiens mRNA for cylicin II//0.0061:287:60//Hs.3232:Z4  
 6788  
 F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.  
 51048:X68830  
 F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:  
 72//Hs.153014:AB002353  
 F-THYRO1001100//Human DNA-binding protein mRNA, 3' end//2.1e-74:741:74//H  
 s.159249:Z99130  
 F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447  
 :62//Hs.124024:AF053700

F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416  
 F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425  
 F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074  
 F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788  
 F-THYRO1001173  
 F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385  
 F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163  
 F-THYRO1001204  
 F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.  
 .155464:AF088219  
 F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461  
 F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.  
 6467:AJ002309  
 F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds  
 //0.014:178:66//Hs.125315:AF027156  
 F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836  
 F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182  
 F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872  
 F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68/  
 /Hs.153563:AF011333  
 F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545  
 F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207  
 F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939  
 F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79  
 //Hs.12385:AB007877  
 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4  
 e-157:740:97//Hs.138488:AB014607  
 F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993  
 F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946

F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694  
F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62  
//Hs.477:U05659  
F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788  
F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' f  
lanking sequence//4.6e-33:153:81//Hs.102877:U41315  
F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099  
F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71/  
/Hs.44782:Z82215  
F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.  
51048:X68830  
F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943  
F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904  
F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663  
F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211  
F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046  
F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335  
F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//  
Hs.25306:AF070572  
F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27  
655  
F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs  
.75551:L12535  
F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849  
F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071  
F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046  
F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2  
e-13:108:86//Hs.141045:AA191659  
F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter

), member 4//0.099:540:55//Hs.95958:M91463  
 F-THYR01001661//ESTs//0.12:53:92//Hs.151586:W45568  
 F-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59  
 kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089  
 F-THYR01001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF0  
 10238  
 F-THYR01001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.  
 122908:AF070552  
 F-THYR01001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691  
 F-THYR01001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila  
 melanogaster]//2.5e-51:296:92//Hs.3826:U69560  
 F-THYR01001738//EST//6.9e-30:180:94//Hs.58641:W81229  
 F-THYR01001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813  
 F-THYR01001746//EST//0.96:119:63//Hs.144107:AI053590  
 F-THYR01001772//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725  
 F-THYR01001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324  
 F-THYR01001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//  
 Hs.11711:AB002295  
 F-THYR01001828  
 F-THYR01001854//EST//0.038:128:67//Hs.160649:AI241823  
 F-THYR01001895//Intercellular adhesion molecule 1 (CD54), human rhinovir  
 us receptor//9.6e-13:288:65//Hs.51061:M24283  
 F-THYR01001907//EST//1.9e-12:126:80//Hs.139296:AA350198  
 F-VESEN1000122  
 F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885  
 F-Y79AA1000033  
 F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:  
 230:66//Hs.431:L13689

F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:U78521

F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680

F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053

F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0022:684:58//Hs.83190:U29344

F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860

F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.9242:AF081192

F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079

F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623

F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134

F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365

F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919

F-Y79AA1000328

F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:AF071309

F-Y79AA1000346

F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853

F-Y79AA1000355

F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908

F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897

F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs

.155464:AF088219

F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018

F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:AF082516

F-Y79AA1000480

F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871

F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521

F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.1

51555:AF053356

F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:AF068706

F-Y79AA1000574//Human mRNA for GC box binding protein, complete cds//0.95:258:62//Hs.150557:D31716

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:AF091080

F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:AF060503

F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513

F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:98//Hs.83023:AF093670

F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969

F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377

F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067

F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:AF098799

F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231



F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:24  
4:60//Hs.12307:AF056085

F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete  
cds//0.87:466:59//Hs.122967:AF059569

F-Y79AA1000805

F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568

F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2  
cells, mRNA Partial, 2237 nt]//0.0048:630:57//Hs.83190:U29344

F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956

F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368  
:99//Hs.86660:AA398644

F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA,  
3' end//0.14:499:58//Hs.37288:D16815

F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699

F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gam  
ma subunit [R.norvegicus]//6.9e-69:310:94//Hs.76822:AI359536

F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116  
:L04270

F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M238  
92

F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//  
Hs.79706:U53204

F-Y79AA1001023

F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:10  
0//Hs.78489:U63329

F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:  
772:60//Hs.82208:L46590

F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381

F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511

F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047  
F-Y79AA1001078  
F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete c  
ds//6.5e-11:247:66//Hs.55967:AF022654  
F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381  
F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.  
0:155:63//Hs.5444:AB018293  
F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.2019  
1:U76248  
F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646  
F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965  
F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054  
F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U  
48436  
F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85  
279:U34879  
F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequ  
ence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)  
)//4.0e-135:441:97//Hs.23170:AJ005892  
F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240  
F-Y79AA1001299//Human Ini1 mRNA, complete cds//2.2e-116:323:93//Hs.15562  
6:U04847  
F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395  
F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555  
F-Y79AA1001384  
F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.667  
31:U81599  
F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424  
:96//Hs.154221:H23167

F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489

F-Y79AA1001493//SRV (sex determining region Y)-box 4//0.38:311:61//Hs.83  
484:X70683

F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465

F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROT  
EIN [Homo sapiens]//0.95:256:63//Hs.29974:AI360447

F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744

F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659

F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851

F-Y79AA1001581//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//2.5e-0  
5:272:64//Hs.106070:U22398

F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783

F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109

F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426

F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.  
00078:520:57//Hs.12334:AB014583

F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:42  
1:94//Hs.107039:W27244

F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X  
04385

F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta pol  
ypeptide 1//0.88:243:61//Hs.3620:X04526

F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:42  
6:59//Hs.162:X16302

F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877

F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (I  
RAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191

F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:AI018620

F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//H

s.113082:AB007903

F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079

F-Y79AA1001827//ESTs, Weakly similar to Similar to *S.cerevisiae* YD9335.0

3c protein [H.sapiens]//2.9e-62:313:98//Hs.15709:W81213

F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533

F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:14  
2:90//Hs.103349:AI141124

F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:21  
5:67//Hs.104115:X52332

F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62  
//Hs.106387:AF029778

F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173

F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA,  
complete cds//0.98:430:58//Hs.78501:L13720

F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382

F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611

F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943

F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-  
53:348:88//Hs.18122:AI338045

F-Y79AA1002093

F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865

F-Y79AA1002115

F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395

F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:16  
5:90//Hs.6473:AA853955

F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5  
e-05:393:62//Hs.77864:AB014538

F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515

F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillu

s caldotenax]//2.3e-113:568:96//Hs.111637:AA305890  
 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338  
 :73//Hs.26662:U55984  
 F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477  
 F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508  
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:6  
 3//Hs.1560:D42045  
 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1  
 e-176:821:98//Hs.100729:AB014592  
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903  
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2  
 e-160:748:98//Hs.96731:AB014555  
 F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489  
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1  
 e-130:622:97//Hs.30898:AB014534  
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999  
 F-Y79AA1002351//Human high conductance inward rectifier potassium channe  
 l alpha subunit mRNA, complete cds//0.028:587:58//Hs.2363:L36069  
 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377  
 F-Y79AA1002399  
 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569  
 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142  
 F-Y79AA1002431  
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318  
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:  
 263:69//Hs.55452:AC003973  
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765  
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:6  
 1//Hs.162:X16302

【 0 8 2 8 】

相同性検索結果データ 5.

3' 末端クローン配列に対する Human Unigene 相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータの Title、

P 値: 比較配列の長さ (base): 相同性 (%),

トップヒットデータの Accession No. の順に // で区切って記載した。

なお、同一クローンで 5' 末端配列に対応する 3' 末端配列が決定されていないものは空欄とした。相同性のスコアの P 値が 1 より大であった場合はデータは示さない。

R-HEMBA1000005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F5  
4F2.9 IN CHROMOSOME III [Caenorhabditis elegans] //5.6e-93:501:93//Hs.130  
15:AA628434

R-HEMBA1000030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.  
83:314:61//Hs.266:U06233

R-HEMBA1000042//Archain//1.4e-45:282:89//Hs.33642:X81198

R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:7  
2//Hs.154326:D42087

R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243340

R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329

R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788

R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases  
[C.elegans] //4.4e-90:502:90//Hs.55918:AA151667

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1  
e-100:514:94//Hs.27197:AB018340

R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1  
e-45:435:77//Hs.153026:AB014540

R-nnnnnnnnnnnnn//ESTs, Moderately similar to The KIAA0138 gene product is

novel. [H.sapiens]//7.7e-92:428:100//Hs.126925:AA931237  
R-HEMBA1000158  
R-nnnnnnnnnnnnn//ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58  
:91//Hs.5570:AI377863  
R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545  
R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366  
R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927  
R-HEMBA1000201//Human Inil mRNA, complete cds//3.0e-25:137:99//Hs.155626  
:U04847  
R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311  
R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532  
R-nnnnnnnnnnnnn//EST//2.2e-100:498:96//Hs.161570:W80404  
R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70/  
/Hs.127649:AB007874  
R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.  
3e-23:276:75//Hs.5737:AB007944  
R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019  
R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808  
R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424  
R-nnnnnnnnnnnnn//ESTs, Moderately similar to ovarian-specific protein [R.  
norvegicus]//4.9e-14:208:73//Hs.93332:AA811920  
R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485  
R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962  
R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409  
R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0  
:122:67//Hs.129748:AB011099  
R-nnnnnnnnnnnnn//ESTs//7.4e-76:386:97//Hs.22276:AA191323  
R-nnnnnnnnnnnnn//Human Ca2+-dependent activator protein for secretion mRN  
A, complete cds//8.8e-30:160:98//Hs.151301:U36448

R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus] //1.1e-103:489:99//Hs.108881:AI018024

R-nnnnnnnnnnnnn//ESTs//9.3e-99:472:98//Hs.163512:AA903238

R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560

R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//Hs.73614:U83460

R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243

R-HEMBA1000357//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:K00629

R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857

R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938

R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960

R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//Hs.73614:U83460

R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878

R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:AI340248

R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens] //1.1e-44:447:75//Hs.42849:N31920

R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens] //6.1e-92:373:99//Hs.48675:AI005282

R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700

R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140

R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:AJ001189

R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143

R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014

R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349

R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316



R-HEMBA1000460

R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370

R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs  
.155464:AF088219

R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canel protein. [H.sapiens]//1.1e-31  
:181:94//Hs.61454:AA312449

R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528

R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087

R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571

R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318

R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531

R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885

R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414

R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280

R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD  
//4.0e-55:203:92//Hs.155510:U15782

R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.99722:AI422277

R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809

R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//  
Hs.91916:AF035317

R-nnnnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699

R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881

R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:W74481

R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196

R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128

R-nnnnnnnnnnnnn

R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788  
R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944  
R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//3.9e-113:591:94//Hs.155218:AJ007509  
R-HEMBA1000592//TYROSINE-PROTEIN KINASE ITK/TSK//0.024:309:61//Hs.89519:L10717  
R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041  
R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.158334:U86136  
R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424  
R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438  
R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:AA643235  
R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:AB014590  
R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390  
R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929  
R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136  
R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922  
R-HEMBA1000682//ESTs, Weakly similar to putative p150 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:AI141736  
R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:AF057280  
R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672  
R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213  
R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/

isomerases [C.elegans]//7.2e-113:572:95//Hs.28644:AI018612  
R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:44  
9:75//Hs.74478:U33931  
R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777  
R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110  
R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs  
.155464:AF088219  
R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131  
R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete  
cds//1.6e-32:309:75//Hs.10458:AF088219  
R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612  
R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8  
2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and anti  
body IA4))//1.3e-48:284:90//Hs.103458:X53795  
R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:8  
7//Hs.154326:D42087  
R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939  
R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027  
R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM  
160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977  
R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410  
:77//Hs.154103:AF061258  
R-HEMBA1000851  
R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)  
//3.7e-33:284:80//Hs.159608:U46689  
R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:AI265794  
R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202  
R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608  
R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951

R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219

R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:AI203154

R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672

R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508

R-HEMBA1000919

R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597

R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619

R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:AB018291

R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074

R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:81//Hs.5247:AF029750

R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362:84//Hs.159187:AB007977

R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:AI363498

R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.44766:AJ007590

R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:AI018170

R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878

R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.147434:AI214464

R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902

R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:AI281881

R-HEMBA1001007

R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764

R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:100//Hs.128738:AA970836

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587:95//Hs.158287:AB007937

R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:  
95//Hs.58393:X05360

R-HEMBA1001020//ESTs//0.52:86:72//Hs.69683:AA115292

R-HEMBA1001022//ESTs//3.4e-18:102:100//Hs.63243:AI123912

R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336

R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:AI345543

R-nnnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616

R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4  
e-21:186:79//Hs.132942:AB014521

R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886

R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813

R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X1442  
0

R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0492//2.7e-21:417:64//Hs.127338:AB007961

R-HEMBA1001080

R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788

R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674

R-HEMBA1001094

R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245

R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs  
.155464:AF088219

R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974

R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320

R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879  
:M15530

R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341

R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265

R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs

.155464:AF088219

R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING

ENTRY !!!! [H.sapiens] //1.1e-39:309:82//Hs.96337:AA225358

R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA

0492//0.21:238:60//Hs.127338:AB007961

R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896

R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothet

ical protein 5 [H.sapiens] //0.27:305:62//Hs.100238:U69194

R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:33

3:81//Hs.113283:AF018080

R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316

R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens] //2.9e-20:160:87

//Hs.103102:W55932

R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728

R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435

R-nnnnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae] //2.4e-35:23

9:87//Hs.103919:AA159181

R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674

R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534

R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324

R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs

.155464:AF088219

R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:

89:68//Hs.20912:AB012162

R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214

R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019

R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977

R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950

R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN

FAB1-PES4 INTERGENIC REGION [*S.cerevisiae*] //1.3e-77:458:92//Hs.9398:N418

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R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259

R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:24  
9:78//Hs.113283:AF018080

R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816

R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837

R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334

R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550

R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458

R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482

R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439

R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204

R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081

R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714

R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364

R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199

R-HEMBA1001415

R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:  
183:82//Hs.42674:U61981

R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704

R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263

R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982

R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546

R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077

R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7  
e-47:304:88//Hs.23094:M19503

R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220